

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 22, 2003, 16:07:12 ; Search time 357 Seconds
(without alignments)
8672.984 Million cell updates/sec

Title: US-10-049-742-22

Perfect score: 1147

Sequence: 1 gccttggtcaagcagaata.....gcctcctgagtagctggat 1147

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 2552756 seqs, 1349719017 residues

Word size : 0

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : N Geneseq 19Jun03:*

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21: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA2000.DAT.*
22: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT.*
23: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.*
24: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*
25: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1147	100.0	1147	22	AAF54994 Nucleotide sequenc
2	1096	95.6	2279	24	ABL55114 Human cDNA sequenc
3	994	86.7	3286	24	ABL56700 Nucleotide sequenc
4	634	55.3	754	20	AA234492 Human LYST interrac
5	634	55.3	754	24	ABX04184 Human mRNA differe
6	634	55.3	754	24	ABX76460 cDNA encoding huma
7	453	39.5	7453	22	AAS30481 DNA encoding novel
8	453	39.5	7453	22	AAL06261 Human reproductive

9	450	39.2	747	22	AA196802 Human neuroblastom
10	258	22.5	884	24	ABL55114 Human cDNA sequenc
11	145	12.6	2277	22	AAK68770 Human immune/haema
12	130	11.3	339	24	ABL5522 Human ovarian canc
13	108	9.4	256	24	ABQ56856 Nucleotide sequenc
14	89	7.8	11674	21	AA236210 Nucleotide sequenc
15	89	7.8	12119	22	AA236210 Nucleotide sequenc
16	89	7.8	12578	21	AA236196 Nucleotide sequenc
17	89	7.8	12734	24	ABA95615 Chimeric BVDV/HCV
18	89	7.8	12842	21	AA236203 Nucleotide sequenc
19	89	7.8	13198	21	AA236211 Nucleotide sequenc
20	89	7.8	14078	21	AA238807 Plasmid pBVDDN1, c
21	89	7.8	14578	21	AA248136 Bovine viral diarr
22	89	7.8	15065	21	AA236195 Nucleotide sequenc
23	89	7.8	16622	21	AA236212 Nucleotide sequenc
24	79	6.9	330	16	AAT24617 Human gene signatu
25	44	3.8	72604	20	AA210752 Genomic sequence o
26	44	3.8	72604	24	ABK43231 Human HKNG1 gene.
27	42	3.7	5862	22	AAL04575 Human reproductive
28	42	3.7	5862	23	ABU97582 Human testicular a
29	42	3.7	28001	24	ABS54410 Human immune/haema
30	42	3.7	28001	25	ABX93300 Human prostate exp
31	42	3.7	32249	22	AAL04576 cDNA sequence #514
32	42	3.7	32249	23	ABL97583 Human low adenosin
33	42	3.7	35959	22	AAK78275 Human adenosine re
34	41	3.6	428	23	ABV05272 Human low adenosin
35	40	3.5	1116	24	ABK36123 Human adenosine re
36	40	3.5	1650	21	AA21035 Human cDNA differe
37	40	3.5	1650	21	AA21035 Human pancreatic c
38	40	3.5	13548	21	AA21037 Oesophagus cancer
39	40	3.5	13548	21	AA21037 DNA encoding novel
40	40	3.5	220895	24	ABK84798 Human breast cance
41	39	3.4	267	24	ABV98317 Human breast cance
42	39	3.4	431	24	ABU67608 Human breast cance
43	39	3.4	436	23	AA575409 Human breast cance
44	39	3.4	445	22	AAL25436 Human breast cance
45	39	3.4	458	22	AAL07690 Human breast cance

ALIGNMENTS

RESULT 1

AAF54994

ID AAF54994 standard; DNA; 1147 BP.

XX AAF54994;

XX AAF54994;

DT 15-MAY-2001 (first entry)

XX Nucleotide sequence of a human chaperone polypeptide.

DE Human; chaperone polypeptide; reproductive disease; prolactin production;

XX Human; chaperone polypeptide; reproductive disease; prolactin production;

XX Infertility; tumour; cancer; Peyronie's disease; eye disorder; glaucoma;

XX conjunctivitis; keratitis; neuromuscular disorder; cystic fibrosis;

XX metabolic disorder; Zellweger syndrome; Addison's disease; iritis;

XX autoimmune disorder; inflammatory disorder; systemic lupus erythematosus;

XX acquired immunodeficiency syndrome; AIDS; asthma; atherosclerosis;

XX cell proliferative disorder; gene therapy; ss.

XX Homo sapiens.

OS Homo sapiens.

FH Key

FT CDS

FT Location/Qualifiers

FT 98..907

FT /*tag= a

FT /product= "chaperone protein"

FT WO200109178-A2.

XX 08-FEB-2001.

XX 03-AUG-2000; 2000WO-US21313.

PR 03-AUG-1999; 99US-0146908.
PR 22-OCT-1999; 99US-0160924.
XX (INCY-) INCYTE GENOMICS INC.
XX Yue H, Bandman O, Tang YT, Baughn MR, Azimzai Y, Lu DAM;
PI WPI; 2001-159853/16.
XX P-PSDB; AAB67455.
DR New human chaperone proteins and polynucleotides, useful in diagnosing,
XX treating and preventing reproductive, eye, neuromuscular, metabolic,
XX autoimmune or inflammatory disorders
XX Claim 5; Page 95-96; 102pp; English.
XX The present sequence encodes a human chaperone polypeptide. Human
XX chaperone polypeptides and polynucleotides are useful in the diagnosis,
XX treatment and prevention of reproductive (e.g. prolactin production,
XX infertility, endometrial or ovarian tumour, cancer of the breast,
XX prostate or testis, Peyronie's disease), eye (e.g. conjunctivitis,
XX keratitis, iritis, glaucoma), neuromuscular, metabolic (e.g. Zellweger
XX syndrome, Addison's disease, cystic fibrosis), and autoimmune and
XX inflammatory disorders (e.g. systemic lupus erythematosus, acquired
XX immunodeficiency syndrome (AIDS), asthma, atherosclerosis), infectious
XX or viral diseases, and cell proliferative disorders. Chaperone
XX polynucleotides may be used for somatic or germline gene therapy, to
XX detect and quantify gene expression in biopsied tissues in which
XX expression is correlated with disease.
XX Query Match 100.0%; Score 1147; DB 22; Length 1147;
XX Best Local Similarity 100.0%; Pred. No. 0;
XX Matches 1147; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCCTTGGGTCAAGCAGAAATTAATAGGAGGGGAATGACCTGTAGTGTGGCGGCTA 60
DB 1 GCCTTGGGTCAAGCAGAAATTAATAGGAGGGGAATGACCTGTAGTGTGGCGGCTA 60
QY 61 CTGCCAGCCTGAAGAGGAGTGGCTGACTCTTGACCTGGCTGGGGTTCCTGAGGATGA 120
DB 61 CTGCCAGCCTGAAGAGGAGTGGCTGACTCTTGACCTGGCTGGGGTTCCTGAGGATGA 120
QY 121 GCTAAACCCCTTCCATGTACTGGGGTGGAGCCACAGCATCAGATGTTGAATGAAGAA 180
DB 121 GCTAAACCCCTTCCATGTACTGGGGTGGAGCCACAGCATCAGATGTTGAATGAAGAA 180
QY 181 GGCCCTATAGACAGCTGGCAGTGTGTTTCATCCTGACAAAATCATCATCCCCGGCTGA 240
DB 181 GGCCCTATAGACAGCTGGCAGTGTGTTTCATCCTGACAAAATCATCATCCCCGGCTGA 240
QY 241 GGAGGCTTCAAGGTTTGGGAGCAGCTTGGGACATTTGTCAGCAATGCTGAAAGCGAAA 300
DB 241 GGAGGCTTCAAGGTTTGGGAGCAGCTTGGGACATTTGTCAGCAATGCTGAAAGCGAAA 300
QY 301 GGAGTATGAGATGAACCAATAGGAGGAGTGGCTGAGCGGTCAGTAAATGAGTTTCT 360
DB 301 GGAGTATGAGATGAACCAATAGGAGGAGTGGCTGAGCGGTCAGTAAATGAGTTTCT 360
QY 361 GTCCAAAGCTGAGATGACCTCAAGGAGGCAATGAATGATGTTAGCCGATGCCA 420
DB 361 GTCCAAAGCTGAGATGACCTCAAGGAGGCAATGAATGATGTTAGCCGATGCCA 420
QY 421 AGGAAGCATAGAGGTTTGAATGAGCCGGGAACCTAAGAGTGCAGATCTGTGCTGA 480
DB 421 AGGAAGCATAGAGGTTTGAATGAGCCGGGAACCTAAGAGTGCAGATCTGTGCTGA 480
QY 481 GTGTAATAGGCTGCATCTCTGCTGAGGAAGGAGACTTTGGGAGAGTCAAGCATGTTGG 540
DB 481 GTGTAATAGGCTGCATCTCTGCTGAGGAAGGAGACTTTGGGAGAGTCAAGCATGTTGG 540
QY 541 CCTCAAGATCACTCTTTGGCACTGATGGTGAAGAGGTGTATGACATCACAGAGTGGGC 600

DB 541 CCTCAAGATCACCTACTTTGGCACTGATGGATGGAAGGTGTATGACATCACAGAGTGGGC 600
QY 601 TGGATGCCAGCGTGTAGGTATCTCCCCAGATACCCACAGAGTCCCTATCACATCTCAT 660
DB 601 TGGATGCCAGCGTGTAGGTATCTCCCCAGATACCCACAGAGTCCCTATCACATCTCAT 660
QY 661 TGGTTCTCGGATTCACAGGACCCAGAGGCGGAGAGCCACCCAGATGCCCTCTCTGC 720
DB 661 TGGTTCTCGGATTCACAGGACCCAGAGGCGGAGAGCCACCCAGATGCCCTCTCTGC 720
QY 721 TGAATCTTCAGGATTTCTTGAAGTACCCAGAGTCCCTGAGGAGTGCCTTAAGCCCAAC 780
DB 721 TGAATCTTCAGGATTTCTTGAAGTACCCAGAGTCCCTGAGGAGTGCCTTAAGCCCAAC 780
QY 781 GAACTTCTTTGAGCTCTCAGCCTGCGCTGAGGCGGCTGAGGCTTAAGCCCAAC 840
DB 781 GAACTTCTTTGAGCTCTCAGCCTGCGCTGAGGCGGCTGAGGCTTAAGCCCAAC 840
QY 841 CACAGTACCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 900
DB 841 CACAGTACCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 900
QY 901 AGCTTGTAGTCCCT 960
DB 901 AGCTTGTAGTCCCT 960
QY 961 AGGATCGAGTGTGATTTATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1020
DB 961 AGGATCGAGTGTGATTTATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1020
QY 1021 TATTTTGTAGTGGAGTCTTGTCTGTGTTGCCAGCTGGAGTGCAGTGTGATCTCAG 1080
DB 1021 TATTTTGTAGTGGAGTCTTGTCTGTGTTGCCAGCTGGAGTGCAGTGTGATCTCAG 1080
QY 1081 CTACTGCAACCTCTGTCTCCCGGTTCAAGCAATCTCCATCTCAGCCTCTCTGAGTAG 1140
DB 1081 CTACTGCAACCTCTGTCTCCCGGTTCAAGCAATCTCCATCTCAGCCTCTCTGAGTAG 1140
QY 1141 CTGGGAT 1147
DB 1141 CTGGGAT 1147
RESULT 2
ABL55088
ID ABL55088 standard; DNA; 2279 BP.
XX ABL55088;
XX 08-OCT-2002 (first entry)
DE Human cDNA sequence #1 from clone HNTPB82.
XX Human; HNTPB82; secreted protein; immunosuppressive; food preservative;
XX antiarthritic; antirheumatic; antiproliferative; cytostatic; cardiac;
XX vasotropic; cerebroprotective; neurotropic; neuroprotective; antibacterial;
XX virucide; fungicide; ophthalmological; vulnery; gene therapy; ELISA;
XX radioimmunoassay; enzyme linked immunosorbent assay; autoimmune disease;
XX hyperproliferative disorder; cardiovascular disorder; angiogenesis;
XX cerebrovascular disorder; nervous system disorder; ocular disorder;
XX wound healing; food additive; ss.
XX Homo sapiens.
OS Location/Qualifiers
FH Key 36..1274
FT CDS /*tag= a
FT sig_peptide /*tag= b
FT mat_peptide 39..1271 /*tag= c
XX

PN WO200222638-A1.
XX 21-MAR-2002.
XX 17-JAN-2001; 2001WO-US01386.
XX 12-SEP-2000; 2000US-232104P.
XX (HUMA-) HUMAN GENOME SCI INC.
XX Rosen CA, Komatsoulis GA, Baker KP, Birse CE, Soppet DR, Olsen HS;
PI Moore PA, Wei P, Ebner R, Duan DR, Shi Y, Choi GH, Fiscella M;
PI Ni J;
XX WPI; 2002-258041/30.
DR P-PSDB; ABB77019.
XX
XX New nucleic acid molecules encoding 22 human secreted proteins for
PT diagnosing or treating e.g. autoimmune diseases, hyperproliferative
PT disorders, and cardiovascular disorders, and used as food additives or
PT preservatives -
XX
XX PS Disclosure; Page 451-452; 526pp; English.
XX
XX The sequence represents a cDNA sequence of the invention, isolated
CC from human clone ID HNPB82. The invention relates to novel
CC isolated nucleic acid molecules encoding 22 human secreted proteins. The
CC proteins of the invention have immunosuppressive, antiarthritic,
CC antiinflammatory, antiproliferative, cytostatic, cardiant, vasotropic,
CC cerebroprotective, nootropic, neuroprotective, antibacterial, virucide,
CC fungicide, ophthalmological, and vulnary activity. The polynucleotides
CC may have a use in gene therapy. The polynucleotides and polypeptides
CC encoded by them are used to prevent, treat or ameliorate a medical
CC condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs,
CC chickens or sheep. The polynucleotides and polypeptides are also used in
CC diagnosing a pathological condition or susceptibility to a pathological
CC condition. The antibodies to the proteins can also be used in alleviating
CC symptoms associated with the disorders and in diagnostic immunoassays
CC e.g. radioimmunoassays or enzyme linked immunosorbent assays (ELISA).
CC Disorders which are diagnosed or treated include autoimmune diseases,
CC hyperproliferative disorders, cardiovascular disorders, cerebrovascular
CC disorders, angiogenesis, nervous system disorders, infections caused by
CC bacteria, viruses and fungi and ocular disorders. The polypeptides can
CC also be used to aid wound healing and epithelial cell proliferation. The
CC polypeptides can also be used as a food additive or preservative.
XX
XX Sequence 2279 BP; 540 A; 518 C; 507 G; 614 T; 0 other;
SQ

Query Match 95.6%; Score 1096; DB 24; Length 2279;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1146; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCCTTGGGTCAAGCAGAAATATTATAGCGGGGAATGCACCTGTAGCTAGTGGGCTA 60
Db 368 GCCTTGGGTCAAGCAGAAATATTATAGCGGGGAATGCACCTGTAGCTAGTGGGCTA 427
Qy 61 CTGCGACCGCTCAAGCAGAAATGCTTCCACTTTCACCATGCTGGGGTTCCTGAGATGA 120
Db 428 CTGCGACCGCTCAAGCAGAAATGCTTCCACTTTCACCATGCTGGGGTTCCTGAGATGA 487
Qy 121 GCTAAACCCCTTTCCATGTAAGTGGGGTTGAGGGCCACAGCATCAGATGTTCAACTGAAGAA 180
Db 488 GCTAAACCCCTTTCCATGTAAGTGGGGTTGAGGGCCACAGCATCAGATGTTCAACTGAAGAA 547
Qy 181 GGCTATAGACAGCTGCAGTGTGTTTCATCTTCCTGACAAATAATCATCATCCCCGGGCTGA 240
Db 548 GGCTATAGACAGCTGCAGTGTGTTTCATCTTCCTGACAAATAATCATCATCCCCGGGCTGA 607
Qy 241 GGAGCCCTTCAAGTGTGGAGCAGCTTGGGACATGTGAGCAATGCTGAAAGCGAAA 300
Db 608 GGAGCCCTTCAAGTGTGGAGCAGCTTGGGACATGTGAGCAATGCTGAAAGCGAAA 667
Qy 301 GGAGTATGAGATGAACGAATGGCAGAGATGAGCTGAGCGGCTCAGTAATGAGTTCT 360

Db 668 GGAGTATGAGATGAACGAATGGCAGAGATGAGCTGAGCGGTGAGTAATGAGTTCT 727
Qy 361 GTCCAAAGCTGCAAGATGACCTCAAGAGGCAATGAATATCTATGATGTGTAGCGGATGCCA 420
Db 728 GTCCAAAGCTGCAAGATGACCTCAAGAGGCAATGAATATCTATGATGTGTAGCGGATGCCA 787
Qy 421 AGAAAGCATAGGAGGTTTGAATGACCGGGAACCTAAGAGTGCACAGATCTGTGCTGA 480
Db 788 AGAAAGCATAGGAGGTTTGAATGACCGGGAACCTAAGAGTGCACAGATCTGTGCTGA 847
Qy 481 GTGTAATAGGCTCATCTCTGCTGAGGAAGAGAGATTTTGGGCGAGAGTCAAGCATGTTGGG 540
Db 848 GTGTAATAGGCTCATCTCTGCTGAGGAAGAGAGATTTTGGGCGAGAGTCAAGCATGTTGGG 907
Qy 541 CCTCAAGATCACCTACTTTCGACTGATGGAAGAGGTGTATGACATCACAGAGTGGGC 600
Db 908 CCTCAAGATCACCTACTTTCGACTGATGGAAGAGGTGTATGACATCACAGAGTGGGC 967
Qy 601 TGATGCCAGCGTGTAGGTATCTCCAGATACCCACAGAGTCCCTATCACATCTCAAT 660
Db 968 TGGATGCCAGCGTGTAGGTATCTCCAGATACCCACAGAGTCCCTATCACATCTCAAT 1027
Qy 661 TGGTTCTGGATTCCAGGACACAGAGGGGGGAGAGGACCCAGATGCCCCCTCTCTGC 720
Db 1028 TGGTTCTGGATTCCAGGACACAGAGGGGGGAGAGGACCCAGATGCCCCCTCTCTGC 1087
Qy 721 TGATCTTCAGGATTTCTTGAGTCGGATCTTCAAGTACCCCGAGGAGATGCCCAATGG 780
Db 1088 TGATCTTCAGGATTTCTTGAGTCGGATCTTCAAGTACCCCGAGGAGATGCCCAATGG 1147
Qy 781 GAATCTTCTTGAGCTCCTCAGCTGCCCTCGAGCGGCTGAGCGGCTCTAAGGCCCAACAG 840
Db 1148 GAATCTTCTTGAGCTCCTCAGCTGCCCTCGAGCGGCTGAGCGGCTCTAAGGCCCAACAG 1207
Qy 841 CACAGTACCAAGGGAGAGCCAACTTAAGCGGGGAGAAAGTGAAGAGGAGGCTGTAGCAC 900
Db 1208 CACAGTACCAAGGGAGAGCCAACTTAAGCGGGGAGAAAGTGAAGAGGAGGCTGTAGCAC 1267
Qy 901 AGTTCATGCCCTTCTCTTCTCTCAATCAATGTGAGGAGTCAAAAGGGCTGTAGCAC 960
Db 1268 AGTTCATGCCCTTCTCTTCTCTCAATCAATGTGAGGAGTCAAAAGGGCTGTAGCAC 1327
Qy 961 AGGATCGAGTTGATTTATCTCTCCCTCCCGAGCAGCTAGGAGTCAATCTTTCTTTT 1020
Db 1328 AGGATCGAGTTGATTTATCTCTCCCTCCCGAGCAGCTAGGAGTCAATCTTTCTTTT 1387
Qy 1021 TATTTTTCAGATGAGTCTTCTCTGTTGCCAGCTGGAGTGCAGTGTGATCTCAG 1080
Db 1388 TATTTTTCAGATGAGTCTTCTCTGTTGCCAGCTGGAGTGCAGTGTGATCTCAG 1447
Qy 1081 CTCTACTGCAACCTCTGTCTCCCGGGTTCAAGCAATTTCTCCATCTCAGCTCTCTGAGTAG 1140
Db 1448 CTCTACTGCAACCTCTGTCTCCCGGGTTCAAGCAATTTCTCCATCTCAGCTCTCTGAGTAG 1507
Qy 1141 CTGGGAT 1147
Db 1508 CTGGGAT 1514

RESULT 3
ABL56700
ID ABL56700 standard; cDNA; 3286 BP.
XX
XX ABL56700;
XX AC
XX 30-JUL-2002 (first entry)
XX
XX Nucleotide sequence of human P125-77.22 polypeptide.
XX Human; P125-77.22; mucosal disease; BVDV infection; gene therapy;
XX Gene; ss.
XX

	QY	541	CCTCAAGATCACCTACTTTGCACTGTGAATCGAAAGGTGTATGACATCACAAGTGGGC	800
	Db	1864	CCTCAAGATCACCTACTTTGCACTGTGAATCGAAAGGTGTATGACATCACAAGTGGGC	1923
	QY	601	TGGATGCCAGCGTGTAAGTATCTCCACAGATACCACAGAGTCCCCTATCACATCTCAT	660
	Db	1924	TGGATGCCAGCGTGTAAGTATCTCCACAGATACCACAGAGTCCCCTATCACATCTCAT	1983
	QY	661	TGTTCTCGAATTCACAGCACAGAGCGCGCAGAGCCACCCAGATGCCCTCTCTGC	720
	Db	1984	TGTTCTCGAATTCACAGCACAGAGCGCGCAGAGCCACCCAGATGCCCTCTCTGC	2043
	QY	721	TGATCTTCAGGATTCTTTGAGTCGGATCTTTCAAGTAGCCCCAGGCGAGATGCCCAATGG	780
	Db	2044	TGATCTTCAGGATTCTTTGAGTCGGATCTTTCAAGTAGCCCCAGGCGAGATGCCCAATGG	2103
	QY	781	GAACTTCTTTTCAGCTCTCTCAGCCTGCCCCTGGAGCCGCTGCAGCCTCTTAAGCCCCAACAG	840
	Db	2104	GAACTTCTTTTCAGCTCTCTCAGCCTGCCCCTGGAGCCGCTGCAGCCTCTTAAGCCCCAACAG	2163
	QY	841	CACAGTACCCAGGAGAGAACCAAACCTTAAGCGCGGAAGAAGTGAGGAGGCCCTTCCA	900
	Db	2164	CACAGTACCCAGGAGAGAACCAAACCTTAAGCGCGGAAGAAGTGAGGAGGCCCTTCCA	2223
	QY	901	AGTTTGATGCCCTTCTCTTCTCAAAATCAATGTCAAGGAGTCAAAGGCGTGTAGCAC	960
	Db	2224	AGTTTGATGCCCTTCTCTTCTCAAAATCAATGTCAAGGAGTCAAAGGCGTGTAGCAC	2283
	QY	961	AGGATGGAGTTGATTTATCCCTCTCCCCCAACACCTAGGAAGTGAATCTTTTTCTTTT	1020
	Db	2284	AGGATGGAGTTGATTTATCCCTCTCCCCCAACACCTAGGAAGTGAATCTTTTTCTTTT	2343
	QY	1021	TATTTTGTAGATGGAGTGTCTGTCTGTGCCAGCTGGAGTGGTGTGATCTCAG	1080
	Db	2344	TATTTTGTAGATGGAGTGTCTGTCTGTGCCAGCTGGAGTGGTGTGATCTCAG	2403
	QY	1081	CTTACTGCAACTCTGTCTCCCGGGTTCAAGCAATTTCCCATCTCAGCTCCTGAGTAG	1140
	Db	2404	CTTACTGCAACTCTGTCTCCCGGGTTCAAGCAATTTCCCATCTCAGCTCCTGAGTAG	2463
	QY	1141	CTGGGAT 1147	
	Db	2464	CTGGGAT 2470	
<hr/>				
RESULT 4				
ID	AAZ34492 standard; cDNA; 754 BP.			
XX	AAZ34492;			
AC	(first entry)			
XX	Human LYST interacting protein LIP6 cDNA.			
DE	LIP6; human; LYST-2; LYST interacting protein; lysosome; CHS;			
KW	Chediak-Higashi syndrome; autoimmune disease; rheumatoid arthritis;			
KW	systemic lupus erythematosus; inflammatory bowel disease;			
KW	diabetes mellitus; multiple sclerosis; atopic disease; asthma;			
KW	hay fever; rhinitis; urticaria; nasal polyp; cancer;			
KW	neurodegenerative disease; pigmentation disorder; viral disease;			
KW	platelet dysfunction; ss.			
OS	Homo sapiens.			
XX	Key Location/Qualifiers			
FH	11..586			
FT	/*tag= a			
FT	/partial			
XX	MO9951741-A2.			
PN				
XX				

CC immunogen), binding partners of the polypeptides, a method for
CC identifying an agent useful in modulating mesenchymal cell
CC differentiation induction activity of a molecule, a method of diagnosing
CC a condition characterized by aberrant expression of a nucleic acid
CC molecule or its expression product; a method for determining regression,
CC progression or onset of cartilaginous tissue degeneration condition in a
CC subject characterized by aberrant expression of a nucleic acid molecule
CC or its expression product, a method for treating a cartilaginous tissue
CC degeneration condition, a method for treating a subject to reduce the
CC risk of cartilaginous tissue degeneration condition developing in the
CC subject, a method for identifying a candidate agent for treating a
CC cartilaginous tissue degeneration condition, and a solid-phase nucleic
CC acid molecule array consisting essentially of a set of nucleic acid
CC molecule as cited above (or known from known genes shown to be
CC differentially expressed in developing mesenchymal cells using the
CC technique of representational difference analysis, RDA), its expression
CC products or fragments, fixed to a solid substrate. The nucleic acids,
CC polypeptides and agents are useful for treating cartilaginous tissue
CC degeneration conditions such as osteoarthritis, rheumatoid arthritis,
CC gout arthritis, adjuvant arthritis, arthritis deformans, infectious
CC arthritis or ceterochondrosis. The present sequence is a cDNA from
CC a known gene differentially expressed in developing mesenchymal cells.

XX
SQ Sequence 754 BP; 193 A; 185 C; 200 G; 176 T; 0 other;

Query Match 55.3%; Score 634; DB 24; Length 754;
Best Local Similarity 99.9%; Pred. No. 1.9e-298;
Matches 754; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy	301	GGAGTATGAGTAAAGCATGCGAGAGATGAGCTGAGCGGCTGAGTAAGTAAAGTTCT	360
Db	1	GGAGTATGAGTAAAGCATGCGAGAGATGAGCTGAGCGGCTGAGTAAGTAAAGTTCT	60
Qy	361	GTCCAGCTCAGATGACCTCAAGGAGGCAATGATATGATGTAGCGGATGCCA	420
Db	61	GTCCAGCTCAGATGACCTCAAGGAGGCAATGATATGATGTAGCGGATGCCA	120
Qy	421	AGGAAGCATAGGAGGTTTGAATGACCGGGAACCTAAGAGTGCAGATACCTGCTGA	480
Db	121	AGGAAGCATAGGAGGTTTGAATGACCGGGAACCTAAGAGTGCAGATACCTGCTGA	180
Qy	481	GTGTAAATAGGCTGCTGCTGAGGAAGGAGACTTTTGGCGAGAGTCAAGCATGTTGGG	540
Db	181	GTGTAAATAGGCTGCTGCTGAGGAAGGAGACTTTTGGCGAGAGTCAAGCATGTTGGG	240
Qy	541	CCTCAAGATCAGTCTTCCAGTATGATGGAAGGTGTATGATCATCACAGATGGGC	600
Db	241	CCTCAAGATCAGTCTTCCAGTATGATGGAAGGTGTATGATCATCACAGATGGGC	300
Qy	601	TGGATGCGAGCGGTAGGTATCTCCCGAGATACCCAGAGTCCCTTATCACATCTCAT	660
Db	301	TGGATGCGAGCGGTAGGTATCTCCCGAGATACCCAGAGTCCCTTATCACATCTCAT	360
Qy	661	TGGTTCTCGGATCCAGGACCGAGAGGCGGCGAGAGCCACCCAGATCCCTCTCTGC	720
Db	361	TGGTTCTCGGATCCAGGACCGAGAGGCGGCGAGAGCCACCCAGATCCCTCTCTGC	420
Qy	721	TGATCTTCAGATTTCTTGAGTCGGATCTTTCAAGTACCCCGAGGCGAGATGCCAATGG	780
Db	421	TGATCTTCAGATTTCTTGAGTCGGATCTTTCAAGTACCCCGAGGCGAGATGCCAATGG	479
Qy	781	GAACTCTTTGACGCTCTCAGCTGCTCCCTGAGCGCGTGCAGCCCTTAAGCCCAACAG	840
Db	480	GAACTCTTTGACGCTCTCAGCTGCTCCCTGAGCGCGTGCAGCCCTTAAGCCCAACAG	539
Qy	841	CACAGTACCCCAAGGAGGAAGCAACCTAAGCGCGGGAAGAGTGAAGGAGGCGCTTCCA	900
Db	540	CACAGTACCCCAAGGAGGAAGCAACCTAAGCGCGGGAAGAGTGAAGGAGGCGCTTCCA	599
Qy	901	ACGTTGATGCCCTTCTCTTCTCAATCAATGTCAGGAGTCAAAAGGCTGTAGCAC	960
Db	600	ACGTTGATGCCCTTCTCTTCTCAATCAATGTCAGGAGTCAAAAGGCTGTAGCAC	659

Qy	961	AGGATGGAGTTTGATTTATCCCTCCTCCCAACACCTAGGAATCTTTTCTTTT	1020
Db	660	AGGATGGAGTTTGATTTATCCCTCCTCCCAACACCTAGGAATCTTTTCTTTT	719
Qy	1021	TATTTTGGAGATGAGTCTTCTGCTGTTGCCAG	1055
Db	720	TATTTTGGAGATGAGTCTTCTGCTGTTGCCAG	754

RESULT 6

ID	ABS76460	ABS76460 standard; cDNA; 754 BP.
XX	XX	ABS76460;
AC	XX	
XX	XX	
DT	11-DEC-2002	(first entry)
XX	XX	
DE	XX	cDNA encoding human ovarian cancer marker OV38.
XX	XX	Human; ovarian cancer; marker; cancer; familial history; brain disorder;
KW	KW	central nervous system disorder; bacterial meningitis; viral meningitis;
KW	KW	Alzheimer's disease; Parkinson's disease; cerebral edema; hydrocephalus;
KW	KW	brain herniation; inflammation; encephalitis; testicular disorder;
KW	KW	nonbacterial granulomatous orchitis; connective tissue disorder;
KW	KW	heart disorder; ischaemic heart disease; atherosclerosis; neoplasm;
KW	KW	histological type; carcinogenic; ovarian cancer marker; gene; ss.
OS	XX	Homo sapiens.
XX	XX	
PN	WO200271928-A2.	
XX	XX	
PD	19-SEP-2002.	
XX	XX	
PF	14-MAR-2002; 2002WO-US07826.	
XX	XX	
PR	14-MAR-2001; 2001US-276025P.	
PR	14-MAR-2001; 2001US-276026P.	
PR	19-AUG-2001; 2001US-311732P.	
PP	19-SEP-2001; 2001US-323580P.	
EX	26-SEP-2001; 2001US-324967P.	
PR	26-SEP-2001; 2001US-325102P.	
PR	26-SEP-2001; 2001US-325149P.	
XX	XX	(MILL-) MILLENNIUM PHARM INC.
XX	XX	Monahan JE, Gannavarapu M, Hoersch S, Kamatkar S, Kovatis SG;
PI	PI	Meyers RE, Morrisey MP, Olandt PJ, Sen A, Wieby PO, Mills GB;
PI	PI	Bast RC, Lu K, Schmandt RE, Zhao X, Glatt K;
XX	XX	WPI; 2002-723277/78.
DR	DR	P-PSDB; ABG96364.
XX	XX	
PT	PT	Assessing whether a patient is afflicted with ovarian cancer, useful in
PT	PT	assessing the stage or progression of the disease, comprises comparing
PT	PT	the expression level of a cancer marker in a sample from a patient and
PT	PT	from a non cancer patient -
XX	XX	
PS	PS	Disclosure; Page 300; 481pp; English.
XX	XX	
CC	CC	The present invention relates to a new method for assessing whether a
CC	CC	patient is afflicted with ovarian cancer. The method involves comparing
CC	CC	the expression level of a marker in a patient sample and the normal level
CC	CC	of expression of the marker in a control non-ovarian cancer sample, where
CC	CC	the marker is selected from 363 cancer markers described in the
CC	CC	specification. The method of the invention is useful in diagnosing or
CC	CC	characterizing cancer, in detecting the presence of cancer as early as
CC	CC	possible, and the recurrence of ovarian cancer. The method may also be of
CC	CC	particular use with patients having an enhanced risk of developing
CC	CC	ovarian cancer (e.g. patients having a familial history of ovarian
CC	CC	cancer). The cancer markers may be used in the management and treatment
CC	CC	of e.g. brain and central nervous system disorders (e.g. bacterial and
CC	CC	viral meningitis, Alzheimer's disease or Parkinson's disease), brain
CC	CC	disorders (e.g. cerebral edema, hydrocephalus or brain herniations),

inflammations (e.g. bacterial or viral meningitis or encephalitis),
testicular disorders (e.g. nontuberculous granulomatous orchitis),
connective tissue disorders, or heart disorders (e.g. ischaemic heart
disease or atherosclerosis). The compositions and methods may also be
used in assessing the histological type of neoplasm associated with
ovarian cancer, monitoring the progression of ovarian cancer,
determining whether ovarian cancer has metastasized or is likely to
metastasize, selecting a composition for inhibiting ovarian cancer,
assessing the ovarian carcinogenic potential of a compound, or
inhibiting ovarian cancer or at risk of developing ovarian cancer. The
present nucleic acid sequence encodes one of the ovarian cancer markers
described in the invention.

Sequence 754 BP; 193 A; 185 C; 200 G; 176 T; 0 other;

Query Match 55.3%; Score 634; DB 24; Length 754;

Best Local Similarity 99.9%; Pred. No. 1.9e-298;

Matches 754; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy	301	GGAGTATGAGATGAAGCAATGGCAGAGATGACCTGAGCGGTCAGTAATGAGTTCT	360
Db	1	GGAGTATGAGATGAAGCAATGGCAGAGATGACCTGAGCGGTCAGTAATGAGTTCT	60
Qy	361	GTCCCAAGCTGCAAGATGACCTCAAGGAGCAATGAATACTATGATGTAGCGGATGCCA	420
Db	61	GTCCCAAGCTGCAAGATGACCTCAAGGAGCAATGAATACTATGATGTAGCGGATGCCA	120
Qy	421	AGGAAGCATGAGGAGTTTGAATGGACCGGAACTTAAGATGCCAGATACCTGTGCTGA	480
Db	121	AGGAAGCATGAGGAGTTTGAATGGACCGGAACTTAAGATGCCAGATACCTGTGCTGA	180
Qy	481	GTGTAATAGGCTGATCCTCTGAGGAAGGAGACTTTGGGCAGAGTCAAGCATGTGGG	540
Db	181	GTGTAATAGGCTGATCCTCTGAGGAAGGAGACTTTGGGCAGAGTCAAGCATGTGGG	240
Qy	541	CCTCAAGATCACCTACTTTGCACTGATGGATGGAAAGGTGTATGACATCAGAGTGGC	600
Db	241	CCTCAAGATCACCTACTTTGCACTGATGGATGGAAAGGTGTATGACATCAGAGTGGC	300
Qy	601	TGGATGCGAGGCTAGTATCTCCAGATACCCAGAGTCCCTATCAGATCTCAT	660
Db	301	TGGATGCGAGGCTAGTATCTCCAGATACCCAGAGTCCCTATCAGATCTCAT	360
Qy	661	TGGTTCTCGATTCCAGSCACAGAGGCGGAGAGCCACCCAGATGCCCTCTCTGC	720
Db	361	TGGTTCTCGATTCCAGSCACAGAGGCGGAGAGCCACCCAGATGCCCTCTCTGC	420
Qy	721	TGATCTTCAGGATTTCTTGAGTCGGATCTTTCAAGTACCCCGGAGATGCCAATGG	780
Db	421	TGATCTTCAGGATTTCTTGAGTCGGATCTTTCAAGTACCCCGGAGATGCCAATGG	479
Qy	781	GAACTCTTTGAGCTCCTCAGCCTGCCCTGGAGCGCTGCAGCCTCTAAGGCCAACAG	840
Db	480	GAACTCTTTGAGCTCCTCAGCCTGCCCTGGAGCGCTGCAGCCTCTAAGGCCAACAG	539
Qy	841	CACAGTACCAAGGAGAGCCAAACCTAAGCGCGGAGAAAGTGAAGGCGCTTCCA	900
Db	540	CACAGTACCAAGGAGAGCCAAACCTAAGCGCGGAGAAAGTGAAGGCGCTTCCA	599
Qy	901	ACGTTGATGCGCTTCTCTTCTCCTCAATCAATGTCAGGAGTCAAAAGGCTGTAGAC	960
Db	600	ACGTTGATGCGCTTCTCTTCTCCTCAATCAATGTCAGGAGTCAAAAGGCTGTAGAC	659
Qy	961	AGGATGAGTTGATTTATCTCCCTCCCAACCTAGGAACTGAATCTTTCTTTT	1020
Db	660	AGGATGAGTTGATTTATCTCCCTCCCAACCTAGGAACTGAATCTTTCTTTT	719
Qy	1021	TATTTTTGAGTGGAGTCTTGCTCTGTTGCCAG 1055	
Db	720	TATTTTTGAGTGGAGTCTTGCTCTGTTGCCAG 754	

RESULT 7

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PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
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PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232397.
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PR 14-SEP-2000; 2000US-0232400.
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PR 20-OCT-2000; 2000US-0241786.
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PR 01-NOV-2000; 2000US-0244617.
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PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 11-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
PI
XX WPI; 2001-476223/51.
DR
XX
XX Novel isolated prostate gland related polypeptide useful for diagnosis
PT and treatment of disorders of prostate such as prostatodystonia,
PT prostatosis, prostatitis, benign prostatic hypertrophy and malacoplakia
PT
XX
XX Claim 1; SEQ ID No 339; 512pp; English.
PS
XX
XX The invention relates to novel isolated prostate gland related nucleic
CC acids (I) and polypeptides (II). (I) and (II) are useful for diagnosis,
CC prognosis, prevention, and/or treatment of diseases and/or disorders of
CC the prostate such as acute non-bacterial prostatitis, chronic non-
CC bacterial prostatitis, acute bacterial prostatitis, prostatodystonia,
CC prostatosis, granulomatous prostatitis, malacoplakia, benign prostatic
CC hypertrophy or hyperplasia, and prostate neoplastic disorders, including
CC adenocarcinomas, transitional cell carcinomas, ductal carcinomas, and
CC squamous cell carcinomas. (I), (II) and antibody to (II) are useful for
CC diagnosing and treating reproductive system disorders (Paget's disease),
CC autoimmune disorders (systemic lupus erythematosus, rheumatoid
CC arthritis), blood-related disorders (sickle cell anemia),
CC hyperproliferative disorders, urinary system disorders
CC (glomerulonephritis), cardiovascular disorders (arrhythmias),
CC respiratory disorders, musculoskeletal system disorders, neural activity
CC and neurological disorders (Alzheimer's disease and Parkinson's disease),
CC endocrine disorders (Addison's disease), gastrointestinal disorders
CC (inflammatory disorders), liver disorders (biliary liver cirrhosis),
CC pancreatic and gall bladder disorders, disorders of the large intestine,
CC developmental and inherited disorders, diseases at the cellular level,
CC and wound healing and epithelial cell proliferation. (I) or (II) is
CC useful to prevent skin aging, for preventing hair loss, to maintain
Query Match 39.5%; Score 453; DB 22; Length 7453;
Best Local Similarity 100.0%; Pred. No. 2.7e-210;
Matches 453; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 695 AGAGCCACCCAGATGCCCTCTCTGCTGATCTTCAGGATTTCTTGATCGGATCTTTCAA 754
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QY 755 GTACCCCGAGGAGATGCCCAATGGAACTTTTTCAGCTCTCAGCTGCCCTGGA 814
DB 3375 GTACCCCGAGGAGATGCCCAATGGAACTTTTTCAGCTCTCAGCTGCCCTGGA 3434
QY 815 GCCGCTGAGCTCTTAAGCCCAACAGCACAGTAGTACCAAGGAGAGCAACCTAACCGG 874
DB 3435 GCCGCTGAGCTCTTAAGCCCAACAGCACAGTAGTACCAAGGAGAGCAACCTAACCGG 3494
QY 875 CGGAAGAAAGTGAGAGGCCCTTCCAACTGTGATGCCCTTCTTCTTCTTCAATCAATG 934
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Qy 995 ACCTAGGAACGAAATCTTTTCTTTTATTTTGGATGGAGCTTGTCTGTGGCCA 1054
Db 3615 ACCTAGGAACGAAATCTTTTCTTTTATTTTGGATGGAGCTTGTCTGTGGCCA 3674
Qy 1055 GCTGGAGTGCAGTGGTGTGATCTCAGCTTACTGCAACTCTGTCTCCGGGTTCAAGCA 1114
Db 3675 GCTGGAGTGCAGTGGTGTGATCTCAGCTTACTGCAACTCTGTCTCCGGGTTCAAGCA 3734
Qy 1115 TTCTCCCATCTCAGCTTCTCAGTGTGGAT 1147
Db 3735 TTCTCCCATCTCAGCTTCTCAGTGTGGAT 3767

RESULT 8

AAL06261

ID AAL06261 standard; DNA; 7453 BP.

XX AAL06261;

AC AAL06261;

DT 21-NOV-2001 (first entry)

XX Human reproductive system related antigen DNA SEQ ID NO: 8949.

KW Human; reproductive system related antigen; reproductive system disorder;

KW cancer; gene therapy; ds.

XX Homo sapiens.

XX WO200155320-A2.

XX 02-AUG-2001.

XX 17-JAN-2001; 2001WO-US01339.

XX 31-JAN-2000; 2000US-0179065.

XX 04-FEB-2000; 2000US-0180628.

XX 24-FEB-2000; 2000US-0184664.

XX 02-MAR-2000; 2000US-0186350.

XX 16-MAR-2000; 2000US-0189874.

XX 17-MAR-2000; 2000US-0190076.

XX 18-APR-2000; 2000US-0198123.

XX 19-MAY-2000; 2000US-0205515.

XX 07-JUN-2000; 2000US-0209467.

XX 28-JUN-2000; 2000US-0214886.

XX 30-JUN-2000; 2000US-0215135.

XX 07-JUL-2000; 2000US-0216647.

XX 07-JUL-2000; 2000US-0216880.

XX 11-JUL-2000; 2000US-0217487.

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XX 26-JUL-2000; 2000US-0220963.

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XX 14-AUG-2000; 2000US-0225447.

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XX 18-AUG-2000; 2000US-0226279.

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PR	06-DEC-2000; 2000US-0251479.	
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PR	11-DEC-2000; 2000US-0254097.	
PR	05-JAN-2001; 2001US-0259678.	
XX		
XX	(HUMA-) HUMAN GENOME SCI INC.	
XX	Rosen CA, Barash SC, Ruben SM;	
XX	WPI; 2001-465570/50.	
XX		
PT	Isolated nucleic acid molecule encoding a reproductive system antigen	
PT	is used in preventing, treating or ameliorating a medical condition -	
XX		
XX	Disclosure; SEQ ID NO 8949; 1297pp + Sequence Listing; English.	
XX	The present invention provides the protein and coding sequences of a	
CC	number of human reproductive system related antigens, these can be used	
CC	in the prevention and treatment of reproductive system disorders,	
CC	including cancer. The present sequence is a genomic sequence encoding a	
CC	protein of the invention.	
XX		
SQ	Sequence 7453 BP; 1980 A; 1633 C; 1692 G; 2147 T; 1 other;	
	Query Match 39.5%; Score 453; DB 22; Length 7453;	
	Best Local Similarity 100.0%; Pred. No. 2.7e-210;	
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Qy	695 AGAGCCACCCCAGATGCCCTCGTGTGATCTTCAGGATTCTTGATCGGATCTTTCAA 754	
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Qy	755 GTACCCCCAGGGCAGATGCCAATGGGAAGTCTTTGCAGCTCTCAGCTGCCCTGGA 814	
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Dd	3495 CGGAAGAAAGTAGGAGGCCCTTCCAACGTTGATGCCCTTCTTTCTCTCAATCAATG 3554	
Qy	935 TCAGGAGTCAAAAGGGCTGTAGCACAGGATGAGTTGATTTATCCTCTCTCCCCCAAC 994	

Db 178 GCAATGCTGAAAGCGAAAGAGATATGAGATGAACGAATGGCAGAGAAATGAGCTGAGCC 237
Qy 342 GGTCAAGTAAATGAGTTCTTCTGCAAGCTGCAAGATGACCTCAAGAGGCAATGAATACTA 401
Db 238 GGTCAAGTAAATGAGTTCTGTCGAAGCTGCAAGATGACCTCAAGAGGCAATGAATACTA 297
Qy 402 TGATGTTAGCCGATGCCAAGGAAAGCATAGGAGGTTTGAATGGACCGGAAACCTAAGA 461
Db 298 TGATGTTAGCCGATGCCAAGGAAAGCATAGGAGGTTTGAATGGACCGGAAACCTAAGA 357
Qy 462 GTGCCAGATAGTGTGCTGAGTGAATAGGCTGCATCTGCTGAGGAAGGAGACTTTGGG 521
Db 358 GTGCCAGATAGTGTGCTGAGTGAATAGGCTGCATCTGCTGAGGAAGGAGACTTTGGG 417
Qy 522 CAGAGTCAAGCATGTTGGGCTCAAGATCACTTGTGACATGATGGATGGAAGGTGT 581
Db 418 CAGAGTCAAGCATGTTGGGCTCAAGATCACTTGTGACATGATGGATGGAAGGTGT 477
Qy 582 ATGACATCACAGAGTGGGCTGGATGCCAGC 611
Db 478 ATGACATCACAGAGTGGGCTGGATGCCAGC 507
RESULT 10
ABL55114
ID ABL55114 standard; DNA; 884 BP.
XX AC ABL55114;
XX 08-OCT-2002 (first entry)
XX Human cDNA sequence #2 from clone HNTPB82.
XX Human; HNTPB82; secreted protein; immunosuppressive; food preservative;
KW antiarthritic; antirheumatic; antiproliferative; cytostatic; cardiac;
KW vasotropic; cerebroprotective; neurotropic; neuroprotective; antibacterial;
KW virucide; fungicide; ophthalmological; vulnary; gene therapy; ELISA;
KW radioimmunoassay; enzyme linked immunosorbent assay; autoimmune disease;
KW hyperproliferative disorder; cardiovascular disorder; angiogenesis;
KW cerebrovascular disorder; nervous system disorder; ocular disorder;
wound healing; food additive; ss.
XX Homo sapiens.
XX Key Location/Qualifiers
CDS 272..883
FT /*tag= a
FT /note= "No stop codon given"
FT sig_peptide 272..400
FT /*tag= b
FT mat_peptide 401..883
FT /*tag= c
XX WO20022638-A1.
XX 21-MAR-2002.
XX 17-JAN-2001; 2001WO-US01386.
XX 12-SEP-2000; 2000US-232104P.
XX (HUMA-) HUMAN GENOME SCI INC.
XX Rosen CA, Komatsoulis GA, Baker KP, Birse CE, Soppet DR, Olsen HS;
PI Moore PA, Wei P, Ebner R, Duan DR, Shi Y, Choi GH, Fiscella M;
PI Ni J;
XX WPI; 2002-258041/30.
DR P-PSDB; ABB77045.
XX New nucleic acid molecules encoding 22 human secreted proteins for
PT diagnosing or treating e.g. autoimmune diseases, hyperproliferative

disorders, and cardiovascular disorders, and used as food additives or preservatives -
Disclosure; Page 466-467; 526pp; English.
The sequence represents a cDNA sequence of the invention, isolated from human clone ID HNTPB82. The invention relates to novel isolated nucleic acid molecules encoding 22 human secreted proteins. The proteins of the invention have immunosuppressive, antirheumatic, antirheumatic, antiproliferative, cytostatic, cardiac, vasotropic, cerebroprotective, neurotropic, neuroprotective, antibacterial, virucide, fungicide, ophthalmological, and vulnary activity. The polynucleotides may have a use in gene therapy. The polynucleotides and polypeptides encoded by them are used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. The polynucleotides and polypeptides are also used in diagnosing a pathological condition or susceptibility to a pathological condition. The antibodies to the proteins can also be used in alleviating symptoms associated with the disorders and in diagnostic immunoassays e.g. radioimmunoassays or enzyme linked immunosorbent assays (ELISA). Disorders which are diagnosed or treated include autoimmune diseases, hyperproliferative disorders, cardiovascular disorders, cerebrovascular disorders, angiogenesis, nervous system disorders, infections caused by bacteria, viruses and fungi and ocular disorders. The polypeptides can also be used to aid wound healing and epithelial cell proliferation. The polypeptides can also be used as a food additive or preservative.
Query Match 22.5%; Score 258; DB 24; Length 884;
Best Local Similarity 100.0%; Pred. No. 2.5e-115; Indels 0; Gaps 0;
Matches 258; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GCCTTGGGTCAGCAGAGATATTATAGGAGGGGAATGCACCTGTAGTGGGCGCTA 60
Db 562 GCCTTGGGTCAGCAGAGATATTATAGGAGGGGAATGCACCTGTAGTGGGCGCTA 621
Qy 61 CTGCCAGCTGAAGAGGAGTGCTGCTGCTTGTACCTTGTGGGTTCTTGAGAGTGA 120
[622 CTGCCAGCTGAAGAGGAGTGCTGCTGCTTGTACCTTGTGGGTTCTTGAGAGTGA 681
Qy 121 GCTAAACCTTTCCATGTACTTGGGGTTGAGGCCACAGCATCAGATGTTGAACCTGAAGAA 180
Db 682 GCTAAACCTTTCCATGTACTTGGGGTTGAGGCCACAGCATCAGATGTTGAACCTGAAGAA 741
Qy 181 GGCCTATAGACAGCTGGCAGTGATGTTTCATCTGCACAAAATCATCATCCCCGGCTGA 240
Db 742 GGCCTATAGACAGCTGGCAGTGATGTTTCATCTGCACAAAATCATCATCCCCGGCTGA 801
Qy 241 GGAGGCTTCAAGGTTTT 258
Db 802 GGAGGCTTCAAGGTTTT 819
RESULT 11
AAK68770
ID AAK68770 standard; DNA; 2277 BP.
XX AC AAK68770;
XX 06-NOV-2001 (first entry)
XX Human immune/haematopoietic antigen genomic sequence SEQ ID NO:23582.
XX Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW cytostatic; gene therapy; vaccine; metastasis; ds.
XX Homo sapiens.
XX WO200157182-A2.
PN 09-AUG-2001.
XX

PF 17-JAN-2001; 2001WO-US01354.
XX 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226868.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0234984.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.

PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249246.
PR 17-NOV-2000; 2000US-0249255.
PR 17-NOV-2000; 2000US-0249257.
PR 17-NOV-2000; 2000US-0249259.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 11-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.

(HUMA-) HUMAN GENOME SCI INC.

Rosen CA, Barash SC, Ruben SM;

WPI; 2001-483426/52.

Nucleic acids encoding human immune/hematopoietic antigen polypeptides,

PT useful for preventing, diagnosing and/or treating cancers and
PT metastasis -
XX
PS Disclosure; SEQ ID NO 23582; 3071pp + Sequence Listing; English.
XX
XX AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
CC amino acid sequences given in AAK82170 to AAK91921. (I) have cytostatic
CC activity, and can be used in gene therapy and vaccine production. (I)
CC proteins and polynucleotides may be used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate (I) expression. For
CC example, they may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of (I) by expressing inactive proteins or to
CC supplement the patient's own production of (I). Additionally, (I)
CC polynucleotides may be used to produce the secreted (I), by inserting
CC the nucleic acids into a host cell and culturing the cell to express the
CC protein. (I) proteins and polynucleotides may be used to prevent,
CC diagnose and treat immune/haematopoietic-related diseases, especially
CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703
CC to AAK87694 represent human immune/haematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and AAK82169
CC represent sequences used in the exemplification of the present invention.
XX
SQ Sequence 2277 BP; 479 A; 579 C; 662 G; 557 T; 0 other;
Query Match 12.6%; Score 145; DB 22; Length 2277;
Best Local Similarity 100.0%; Pred. No. 2.7e-60; Indels 0; Gaps 0;
Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCCTTGGGTCAGACAGATATTAATAGGAGGGGAATGACCTGTAGTGGCGCTA 60
DB 2133 GCCTTGGGTCAGACAGATATTAATAGGAGGGGAATGACCTGTAGTGGCGCTA 2192
QY 61 CTGCCAGCCTGAAGAGGAGTGCTCGACTTTGACCATGGCTGGGTTCTTGAGATGA 120
DB 2193 CTGCCAGCCTGAAGAGGAGTGCTCGACTTTGACCATGGCTGGGTTCTTGAGATGA 2252
QY 121 GCTAAACCTTTCCATGCTACTGGG 145
DB 2253 GCTAAACCTTTCCATGCTACTGGG 2277
RESULT 12
ABL85522
ID ABL85522 standard; cDNA; 339 BP.
XX
AC ABL85522;
XX
DT 17-MAY-2002 (first entry)
XX
DE Human ovarian cancer related cDNA clone SEQ ID NO:8500.
XX
KW Human; ovarian cancer; ovarian tumour; cytostatic; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200192581-A2.
XX
PD 06-DEC-2001.
XX
PF 29-MAY-2001; 2001WO-US17756.
XX
PR 26-MAY-2000; 2000US-207484P.
XX
PA (CORI-) CORIXA CORP.
XX
PI Algate PA, Harlocker SL, Jones R;
XX
DR WPI; 2002-122075/16.
XX
PT Composition for therapy and diagnosis of ovarian cancer comprising
PT polypeptide of a ovarian tumor polypeptide, polynucleotide encoding
PT polypeptide, antibody specific to polypeptide or T cell expressing

PT polypeptide -
XX
PS Claim 1; SEQ ID 8500; 489pp; English.
XX
CC The present invention describes a composition (I) comprising: carriers
CC and immunostimulants; and a polypeptide (II) of a ovarian tumour
CC polypeptide encoded by a polynucleotide (III) having a cDNA sequence
CC (S1) from the 10912 nucleotide sequences as given in ABL77023 to
CC ABL7934, (III) encoding (II) having a sequence (S2), a T cell
CC population of (II), or antigen presenting cells that express (II).
CC (I) has cytostatic activity. An oligonucleotide (IV) that hybridises to
CC (S1) can be used for detecting ovarian cancer in a patient's biological
CC sample preferably serum or ovarian tissue. The method comprises
CC contacting a biological sample from a patient with (IV), detecting the
CC amount of polynucleotide hybridising to (IV) and comparing the amount to
CC a predetermined cutoff value and thereby detecting ovarian cancer in the
CC patient, where the amount of polynucleotide hybridising to (IV) is
CC detected preferably by polymerase chain reaction (PCR). (I) comprising
CC (III) and/or (II) is useful for stimulating and/or expanding T cells
CC specific for an ovarian tumour protein comprising contacting T cells
CC with (III) or (II). (III) is useful in design and preparation of
CC ribozyme molecules for inhibiting expression of the tumour polypeptides
CC and proteins in tumour cells; and to isolate a full length gene from a
CC suitable library e.g., a tumour cDNA library using well known
CC techniques.
XX
SQ Sequence 339 BP; 73 A; 76 C; 67 G; 123 T; 0 other;
Query Match 11.3%; Score 130; DB 24; Length 339;
Best Local Similarity 100.0%; Pred. No. 5.6e-53;
Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 899 CAACGTTGATGCCCTTCTCTTCTCAAAATCAATGTCAAGGAGTCAAAAGGCTGTAGC 958
DB 26 CAACGTTGATGCCCTTCTCTTCTCAAAATCAATGTCAAGGAGTCAAAAGGCTGTAGC 85
QY 959 ACAGATGGAGTTGATTTATCCCTCTCCCCCAACCTAGGAACCTGAACTCTTTCTT 1018
DB 86 ACAGATGGAGTTGATTTATCCCTCTCCCCCAACCTAGGAACCTGAACTCTTTCTT 145
QY 1019 TTTATTTTTT 1028
DB 146 TTTATTTTTT 155
RESULT 13
ABQ56856
ID ABQ56856 standard; cDNA; 256 BP.
XX
AC ABQ56856;
XX
DT 02-AUG-2002 (first entry)
XX
DE Human colon cancer related nucleotide sequence SEQ ID NO:551.
XX
KW Human; colon cancer; cancer; tissue profiling; forensic; mapping;
KW genetic analysis; diagnostic; antisense therapy; gene; ss.
XX
OS Homo sapiens.
XX
FN WO200229086-A2.
XX
PD 11-APR-2002.
XX
PF 02-OCT-2001; 2001WO-US30732.
XX
PR 02-OCT-2000; 2000US-237271P.
XX
PA (FARB) BAYER CORP.
XX
XX Burgess C, Astle JH, Carroll E, Catino TJ, Dwivedi P, Molino GA;
PI Thiagalingam A, Lewis ME;
XX

DR WPI; 2002-426115/45.
XX
PT New isolated nucleic acid that is differentially expressed in cancer
PT tissues useful for determining the presence of colon cancer in a cell
PT or tissue type, and in antisense therapy -
XX
PS Claim 1; Fig 1; 796pp; English.
XX
CC ABQ56306 to ABQ60787 represent isolated nucleic acids (I) differentially
CC expressed in cancer tissues. ABB78993 to ABB79004 represent proteins
CC encoded by the ABQ60776 to ABQ60787 nucleic acid sequences. (I) can be
CC used in antisense therapy. An antibody immunoreactive with a polypeptide
CC encoded by (I) is useful for detecting cancer in a patient sample, and
CC for detecting the presence or absence of a polynucleotide encoded by a
CC nucleic acid which hybridises to (I) in a cell. A probe/primer derived
CC from (I) can be used for determining the presence of a nucleic acid which
CC hybridises to (I), and for determining the phenotype of cells in a sample
CC of cells from a patient. (I) is useful for determining the presence of
CC colon cancer in a cell or tissue type, for determining the presence or
CC state of other type of cancer, in antisense therapy, to generate
CC macroarrays on a solid surface, to identify a chromosome on which the
CC corresponding gene resides, and in tissue profiling, for forensic, genetic
CC analysis, mapping and diagnostic applications. (I) can be used to raise
CC antibodies, and to screen for peptide analogues and antagonists.
XX
SQ Sequence 256 BP; 57 A; 64 C; 59 G; 70 T; 6 other;
Query Match 9.4%; Score 108; DB 24; Length 256;
Best Local Similarity 100.0%; Pred. No. 2.9e-42;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 872 CGGCGAAGAAAGTGAAGAGGCGCTTCCAACTTATGATGCCCTTCTTTCTCAATCA 931
DB 26 CGGCGAAGAAAGTGAAGAGGCGCTTCCAACTTATGATGCCCTTCTTTCTCAATCA 85
QY 932 ATGTGAGGAGTCAAAAGGCTGTAGCAGGATGGAGTTGATTAT 979
DB 86 ATGTGAGGAGTCAAAAGGCTGTAGCAGGATGGAGTTGATTAT 133
RESULT 14
AAZ36210
ID AAZ36210 standard; DNA; 11674 BP.
AC AAZ36210;
XX
DT 11-FEB-2000 (first entry)
DE Nucleotide sequence of functional HCV-BVDV chimera from PCBV/p7.
KW Pseudorevertant; RNA virus; chimera; BVDV; HCV; replication-competent;
KW 5' nontranslated region; 5'NTR; 3' NTR; pestivirus; antiviral;
KW bovine viral diarrhoea virus; NADL; vaccine; ss.
OS Chimeric - Hepatitis C virus.
OS Chimeric - Bovine viral diarrhoea virus.
XX WO955366-A1.
XX
PD 04-NOV-1999.
XX
PF 23-APR-1999; 99WO-US08850.
XX
PR 24-APR-1998; 98US-0082964.
XX
XX (UNIW) UNIV WASHINGTON.
XX
PI Rice CM, Frolov I, McBride MS;
XX
XX WPI; 2000-013359/01.
XX
PT Chimeric viral RNA, used in vaccine against BVDV -
XX

PS Disclosure; Fig 22; 108pp; English.
XX
CC The present sequence represents a functional Hepatitis C virus
CC (HCV)-bovine viral diarrhoea virus (BVDV) chimeric virus of the
CC invention. The specification describes chimeric viral RNA comprising a
CC 5' nontranslated region (5'NTR); an open reading frame (ORF) region;
CC and a 3' NTR; where at least one of the regions is chimeric and
CC comprises a nucleotide sequence from a pestivirus in operable linkage
CC with a heterologous nucleotide sequence, preferably from HCV. The
CC chimeric viral RNA is replication-competent. The chimeric viral RNA
CC can be used in a method for identifying compounds having antiviral
CC activity against HCV. When the pestivirus viral nucleotide sequence is
CC from bovine viral diarrhoea virus (BVDV), the chimeric viral RNA can be
CC used in a vaccine against BVDV.
XX
SQ Sequence 11674 BP; 3407 A; 2614 C; 3100 G; 2553 T; 0 other;
Query Match 7.8%; Score 89; DB 21; Length 11674;
Best Local Similarity 100.0%; Pred. No. 5.1e-33;
Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 422 GGAAGCATAGGAGGTTTGAATGGACCGGGAACCTAAGAGTGCCAGATCTGTGCTGAG 481
DB 4109 GGAAGCATAGGAGGTTTGAATGGACCGGGAACCTAAGAGTGCCAGATCTGTGCTGAG 4168
QY 482 TGTAAATAGGCTGCATCTCTGTGAGGAAGG 510
DB 4169 TGTAAATAGGCTGCATCTCTGTGAGGAAGG 4197
RESULT 15
AAC86936
ID AAC86936 standard; DNA; 12119 BP.
AC AAC86936;
XX
DT 02-APR-2001 (first entry)
DE Nucleotide sequence of a chimeric BVDV/HCV virus.
KW Chimeric virus; bovine viral diarrhoea virus; BVDV; hepatitis C virus;
KW HCV; vaccine; viral inhibitor; antiviral; ss.
XX
OS Synthetic.
OS Bovine viral diarrhoea virus.
OS Hepatitis C virus.
XX
PH Key Location/Qualifiers
FT CDS 386..11893
FT /*tag= a
XX
PN WO200075352-A2.
XX
PD 14-DEC-2000.
XX
PF 02-JUN-2000; 2000WO-US15527.
XX
PR 04-JUN-1999; 99US-0137817.
XX
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Nam J, Bukh J, Emerson SU, Purcell RH;
XX
XX WPI; 2001-071081/08.
DR P-PSDB; AAB31167.
XX
PT New nucleic acid comprising a chimeric bovine viral diarrhoea virus
PT genome in which the (non-)structural region has been replaced by
PT hepatitis C virus (HCV) genome useful for treating or preventing HCV
PT signs and symptoms -
XX
PS Disclosure; Page 62-66; 97pp; English.
XX

CC The specification describes a nucleic acid comprising a chimeric virus
CC genome, specifically bovine viral diarrhoea virus (BVDV) genome in which
CC the (non-)structural region has been replaced by the (non-)structural
CC region of a hepatitis C virus (HCV) genome. The nucleic acids comprising
CC the chimeric virus and the chimeric virus are useful for identifying
CC cell lines capable of supporting the replication of these chimeric
CC viruses, in screening for neutralizing antibodies to HCV of different
CC genotypes, in the production of HCV-BVDV virions, for the development
CC of inactivated or attenuated vaccines to prevent HCV-BVDV in a mammal,
CC in studying the molecular properties of HCV indirectly in vitro, and in
CC identifying inhibitors of viral enzyme activity which would be useful
CC as antiviral agents. Formulations or compositions comprising the
CC chimeric virions may be used to treat or prevent the signs and symptoms
CC of HCV. The present sequence represents a chimeric nucleic acid of the
CC invention.

XX
SQ Sequence 12119 BP; 3589 A; 2668 C; 3211 G; 2651 T; 0 other;

Query Match 7.8%; Score 89; DB 22; Length 12119;
Best Local Similarity 100.0%; Pred. No. 5.1e-33;
Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 422 GGAAAGCATAGGAGGTTTGAATGGACCGGGAACCTAAGAGTGCCAGATACCTGTGCTGAG 481
Db 4553 GGAAAGCATAGGAGGTTTGAATGGACCGGGAACCTAAGAGTGCCAGATACCTGTGCTGAG 4612
Qy 482 TGTAAATAGGCTGCATCCTCTGAGGAGG 510
Db 4613 TGTAAATAGGCTGCATCCTCTGAGGAGG 4641

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Job time : 360 secs

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OM nucleic - nucleic search, using sw model

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(without alignments)
9437.129 Million cell updates/sec

Title: US-10-049-742-22

Perfect score: 1147

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Gapop 60.0 , Gapext 60.0

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Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq.*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq.*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq.*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq.*
- 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq.*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq.*
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq.*
- 9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq.*
- 10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq.*
- 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq.*
- 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq.*
- 13: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq.*
- 14: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq.*
- 15: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq.*
- 16: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq.*
- 17: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*
- 18: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1147	100.0	2343	13	US-10-094-749-657
2	1142	99.6	3090	13	Sequence 657, App
3	1047	91.3	2945	15	Sequence 19835, A
4	634	55.3	754	13	Sequence 12415, A
5	634	55.3	754	15	US-10-096-534-43
6	453	39.5	7453	11	US-10-097-340-182
7	276	24.1	443	13	US-09-764-891-8949
8	257	22.4	259	13	Sequence 8949, App
9	257	22.4	259	13	Sequence 14171, A
10	204	17.8	2066	13	US-09-814-353-1471
11	130	11.3	339	10	US-09-814-353-1424
12	89	7.8	12572	15	Sequence 1424, App
13	89	7.8	14078	13	Sequence 7786, App
14	80	7.0	510	13	Sequence 1448, App
15	80	7.0	510	13	Sequence 8500, App
					Sequence 10, Appl
					Sequence 1, Appl
					Sequence 9, Appl
					Sequence 4106, App

C 16	80	7.0	510	13	US-09-814-353-10412	Sequence 10412, A
C 17	80	7.0	598	13	US-09-814-353-16796	Sequence 16796, A
C 18	75	6.5	621	15	US-10-198-846-9074	Sequence 9074, App
C 19	48	4.2	663	13	US-10-027-632-221177	Sequence 221177, A
C 20	48	4.2	663	13	US-10-027-632-221178	Sequence 221178, A
C 21	48	4.2	663	13	US-10-027-632-221177	Sequence 221177, A
C 22	48	4.2	663	13	US-10-027-632-221178	Sequence 221178, A
C 23	44	3.8	72604	14	US-10-162-497-7	Sequence 7, Appl
C 24	43	3.7	108317	13	US-10-017-161-2143	Sequence 2143, App
C 25	42	3.7	836	13	US-10-027-632-119193	Sequence 119193, A
C 26	42	3.7	836	13	US-10-027-632-119193	Sequence 119193, A
C 27	42	3.7	5862	11	US-09-764-891-7363	Sequence 7363, App
C 28	42	3.7	28001	14	US-10-193-295-3	Sequence 3, Appl
C 29	42	3.7	32249	11	US-09-764-891-7364	Sequence 7364, App
C 30	40	3.5	1116	11	US-09-822-846-514	Sequence 514, App
C 31	39	3.4	267	15	US-10-060-036-3725	Sequence 3725, App
C 32	39	3.4	431	10	US-09-962-832-59	Sequence 59, Appl
C 33	39	3.4	650	15	US-10-198-846-7581	Sequence 7581, App
C 34	39	3.4	760	13	US-10-027-632-171114	Sequence 171114, A
C 35	39	3.4	760	14	US-10-027-632-171114	Sequence 171114, A
C 36	39	3.4	907	13	US-10-027-632-259505	Sequence 259505, A
C 37	39	3.4	907	14	US-10-027-632-259505	Sequence 259505, A
C 38	39	3.4	1132	13	US-10-027-632-261923	Sequence 261923, A
C 39	39	3.4	1132	14	US-10-027-632-261923	Sequence 261923, A
C 40	38	3.3	2913	13	US-10-027-632-112023	Sequence 112023, A
C 41	38	3.3	2913	13	US-10-027-632-112024	Sequence 112024, A
C 42	38	3.3	2913	14	US-10-027-632-112023	Sequence 112023, A
C 43	38	3.3	2913	14	US-10-027-632-112024	Sequence 112024, A
C 44	38	3.3	6320	9	US-09-764-878-360	Sequence 360, App
C 45	38	3.3	6320	15	US-10-079-854-360	Sequence 360, App

ALIGNMENTS

RESULT 1

US-10-094-749-657
; Sequence 657, Application US/10094749
; Publication No. US20030219741A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NACHIKO
; APPLICANT: YOSHIZAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOKUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA
; FILE REFERENCE: 084335/0160
; CURRENT APPLICATION NUMBER: US/10/094,749
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 60/350,435
; PRIOR FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: JP 2001-328381
; NUMBER OF SEQ ID NOS: 3381
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 657
; LENGTH: 2343
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-094-749-657

Query Match 100.0%; Score 1147; DB 13; Length 2343; Best Local Similarity 100.0%; Pred. No. 0; Matches 1147; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
Qy	1	GCCTTGGGTCAAGCAGAAATATTAAATAGGAGGGGAATGCACTGTAGTGTGGCGCTA	60						
Db	445	GCCTTGGGTCAAGCAGAAATATTAAATAGGAGGGGAATGCACTGTAGTGTGGCGCTA	504						
Qy	61	CTGCCAGCCTGAAGAGGAAGTGGCTGACTCTTGACCATGGCTGGGTTCTTGAGGATGA	120						
Db	505	CTGCCAGCCTGAAGAGGAAGTGGCTGACTCTTGACCATGGCTGGGTTCTTGAGGATGA	564						
Qy	121	GCTAAACCCCTTCCATGTACTGGGGTTCAGGCCACAGCATCAGATGTTGAACTGAAGAA	180						
Db	565	GCTAAACCCCTTCCATGTACTGGGGTTCAGGCCACAGCATCAGATGTTGAACTGAAGAA	624						
Qy	181	GGCCTATAGACAGCTGGCAGTGTGTTTCCATCTGACAAAATATCATATCCCGGGCTGA	240						
Db	625	GGCCTATAGACAGCTGGCAGTGTGTTTCCATCTGACAAAATATCATATCCCGGGCTGA	684						
Qy	241	GGAGGCTTCAAGGTTTTCGGAGCAGCTTGGGACATTTGACGAATGTCGAAAACGGAAA	300						
Db	685	GGAGGCTTCAAGGTTTTCGGAGCAGCTTGGGACATTTGACGAATGTCGAAAACGGAAA	744						
Qy	301	GGAGTATGATCAGACGATGACGATGACGAGATGAGCTGAGCCGGTCAGTAAATGAGTTCT	360						
Db	745	GGAGTATGATGAGACGATGACGATGAGCTGAGCCGGTCAGTAAATGAGTTCT	804						
Qy	361	GTCCAAAGCTGCAAGATGACTCAAGAGGCAATGAATATGATGATGATGATGATGATGAT	420						
Db	805	GTCCAAAGCTGCAAGATGACTCAAGAGGCAATGAATATGATGATGATGATGATGATGAT	864						
Qy	421	AGGAAAGCATAGAGGTTTGAATGACCGGGAACCTAAGATGCGCAGATCTGTGCTGA	480						
Db	865	AGGAAAGCATAGAGGTTTGAATGACCGGGAACCTAAGATGCGCAGATCTGTGCTGA	924						
Qy	481	GTGTAATAGCTGCATCTCTGAGAGGAGAGACTTTGGGAGAGAGTCAAGCATGTTGG	540						
Db	925	GTGTAATAGCTGCATCTCTGAGAGGAGAGACTTTGGGAGAGAGTCAAGCATGTTGG	984						
Qy	541	CCTCAAGATCACTACTTTGCACTGATGATGAAAGGTGATGACATCAGAGATGGGC	600						
Db	985	CCTCAAGATCACTACTTTGCACTGATGATGAAAGGTGATGACATCAGAGATGGGC	1044						
Qy	601	TGGATGCCAGCTGTAGTATCTCCACAGATACCCACAGAGTCCCTTATCATCTCTATT	660						
Db	1045	TGGATGCCAGCTGTAGTATCTCCACAGATACCCACAGAGTCCCTTATCATCTCTATT	1104						
Qy	661	TGTTTCTCGAATCCAGGACCAAGAGGCGGAGAGAGCCACCCAGATGCCCTCTGC	720						
Db	1105	TGTTTCTCGAATCCAGGACCAAGAGGCGGAGAGAGCCACCCAGATGCCCTCTGC	1164						
Qy	721	TGATCTTCAGGATTTCTTGAGTCGGATCTTCAAGTACCCCGGAGATGCCCAATGG	780						
Db	1165	TGATCTTCAGGATTTCTTGAGTCGGATCTTCAAGTACCCCGGAGATGCCCAATGG	1224						
Qy	781	GAACTCTTTTGAGCTCTCCAGCTCGCCCTGGAGCGCTGAGCGCTCTAAGCCCAACAG	840						
Db	1225	GAACTCTTTTGAGCTCTCCAGCTCGCCCTGGAGCGCTGAGCGCTCTAAGCCCAACAG	1284						
Qy	841	CACAGTACCCAGGAGAGGACCAACCTAAGCGGCGGAGAAAGTGAGGAGGCCCTTCCA	900						
Db	1285	CACAGTACCCAGGAGAGGACCAACCTAAGCGGCGGAGAAAGTGAGGAGGCCCTTCCA	1344						
Qy	901	ACGTTGATGCCCTTCTCTTTTCTCAATGATGTCAGGAGTCAAAAAGGCTGTAGCAC	960						
Db	1345	ACGTTGATGCCCTTCTCTTTTCTCAATGATGTCAGGAGTCAAAAAGGCTGTAGCAC	1404						
Qy	961	AGGATGAGTTGATTTATCTCTCTCCCAACACCTAGGAGTCAATCTTTTCTTTT	1020						
Db	1405	AGGATGAGTTGATTTATCTCTCTCCCAACACCTAGGAGTCAATCTTTTCTTTT	1464						

Qy	1021	TATTTTTGAGATGGAGTCTTGTCTGTTCGCCAGCTGGAGTGAGTGTGATCTCAG	1080						
Db	1465	TATTTTTGAGATGGAGTCTTGTCTGTTCGCCAGCTGGAGTGAGTGTGATCTCAG	1524						
Qy	1081	CTTACTGCAACCTCTGTCTCCCGGTTCAAGCAATCTCCCATCTCAGCCTCCTGAGTAG	1140						
Db	1525	CTTACTGCAACCTCTGTCTCCCGGTTCAAGCAATCTCCCATCTCAGCCTCCTGAGTAG	1584						
Qy	1141	CTGGGAT 1147							
Db	1585	CTGGGAT 1591							
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US-09-814-353-19835/C									
; Sequence 19835, Application US/09814353									
; Publication No. US20030165831A1									
; GENERAL INFORMATION:									
; APPLICANT: Thompson, Pamela									
; APPLICANT: Lillie, James									
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR									
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND									
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER									
; FILE REFERENCE: MRI-006B									
; CURRENT APPLICATION NUMBER: US/09/814,353									
; CURRENT FILING DATE: 2001-03-21									
; PRIOR APPLICATION NUMBER: US 60/191,031									
; PRIOR FILING DATE: 2000-03-21									
; PRIOR APPLICATION NUMBER: US 60/207,124									
; PRIOR FILING DATE: 2000-05-25									
; PRIOR APPLICATION NUMBER: US 60/211,940									
; PRIOR FILING DATE: 2000-06-15									
; PRIOR APPLICATION NUMBER: US 60/215,820									
; PRIOR FILING DATE: 2000-07-07									
; PRIOR APPLICATION NUMBER: US 60/220,661									
; PRIOR FILING DATE: 2000-07-25									
; PRIOR APPLICATION NUMBER: US 60/257,672									
; PRIOR FILING DATE: 2000-12-21									
; NUMBER OF SEQ ID NOS: 22037									
; SOFTWARE: FastSeq for Windows Version 4.0									
; SEQ ID NO 19835									
; LENGTH: 3090									
; TYPE: DNA									
; ORGANISM: Homo sapiens									
; FEATURE:									
; NAME/KEY: misc feature									
; LOCATION: 488..525									
; OTHER INFORMATION: n = A,T,C or G									
US-09-814-353-19835									
Query Match 99.6%; Score 1142; DB 13; Length 3090;									
Best Local Similarity 100.0%; Pred. No. 0;									
Matches 1142; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
Qy	1	GCCTTGGGTCAAGCAGAAATATTAAATAGGAGGGGAATGCACCTGTAGTGTGGCGCTA	60						
Db	1667	GCCTTGGGTCAAGCAGAAATATTAAATAGGAGGGGAATGCACCTGTAGTGTGGCGCTA	1608						
Qy	61	CTGCCAGCCTGAAGAGGAAGTGGCTCGACTTTGACCATGGCTGGGTTCTTGAGGATGA	120						
Db	1607	CTGCCAGCCTGAAGAGGAAGTGGCTCGACTTTGACCATGGCTGGGTTCTTGAGGATGA	1548						
Qy	121	GCTAAACCCCTTCCATGTACTGTTGGGGTTGAGGCCACAGCATCAGATGTTGAACCTGAAGAA	180						
Db	1547	GCTAAACCCCTTCCATGTACTGTTGGGGTTGAGGCCACAGCATCAGATGTTGAACCTGAAGAA	1488						
Qy	181	GGCCTATAGACAGCTGGCAGTGTGTTTCCATCTGACAAAATATCATATCCCGGGCTGA	240						
Db	1487	GGCCTATAGACAGCTGGCAGTGTGTTTCCATCTGACAAAATATCATATCCCGGGCTGA	1428						
Qy	241	GGAGGCTTCAAGGTTTTCGGAGCAGCTTGGGACATTTGAGCAATGCTGAAAACGGAAA	300						

Db 1427 GGAGCCCTCAAGGTTTGGCAGCAGCTTGGGACATGTGACGAATGCTGAAAGCGAAA 1368
Qy 301 GGAGTATGAGATGAACGAATGGCAGAGAAATGAGCTGAGCGCGTCACTAAATGAGTTCT 360
Db 1367 GGAGTATGAGATGAACGAATGGCAGAGAAATGAGCTGAGCGCGTCACTAAATGAGTTCT 1308
Qy 361 GTCCAGCTCAAGATGACCTCAAGGAGGCAATGAATATCTATGATGTGTAGCCGATGCCA 420
Db 1307 GTCCAGCTCAAGATGACCTCAAGGAGGCAATGAATATCTATGATGTGTAGCCGATGCCA 1248
Qy 421 AGGAACCATAGAGGTTTGAATGACCGGAACTTAAGATGACGATGCTGTCTGA 480
Db 1247 AGGAACCATAGAGGTTTGAATGACCGGAACTTAAGATGACGATGCTGTCTGA 1188
Qy 481 GTGTAATAGCTGATCCTCTGAGGAGGAGACTTTTGGCAGAGTCAAGCATGTTGG 540
Db 1187 GTGTAATAGCTGATCCTCTGAGGAGGAGACTTTTGGCAGAGTCAAGCATGTTGG 1128
Qy 541 CCTCAAGATCACCTACTTTGCATCTGATGATGGAAGGTGTATGACATCACAGAGTGGG 600
Db 1127 CCTCAAGATCACCTACTTTGCATCTGATGATGGAAGGTGTATGACATCACAGAGTGGG 1068
Qy 601 TGGATGCCAGCTGTAGTATCTCCAGATACCCACAGAGTCCCTTATCACATCTCAIT 660
Db 1067 TGGATGCCAGCTGTAGTATCTCCAGATACCCACAGAGTCCCTTATCACATCTCAIT 1008
Qy 661 TGGTCTCGAATTCAGGACACAGAGGCGGAGAGGCCACCCAGATGCCCTCTCTGC 720
Db 1007 TGGTCTCGAATTCAGGACACAGAGGCGGAGAGGCCACCCAGATGCCCTCTCTGC 948
Qy 721 TGATCTTCAGATTTCTTGAGTGGATCTTTCAAGTACCCCGAGGCGAGTGGCCAAATGG 780
Db 947 TGATCTTCAGATTTCTTGAGTGGATCTTTCAAGTACCCCGAGGCGAGTGGCCAAATGG 888
Qy 781 GAACTTTCTTGAGCTCCTCAGCCTGCCCCGAGCGCTGAGCGCTCTAAGGCCCAACAG 840
Db 887 GAACTTTCTTGAGCTCCTCAGCCTGCCCCGAGCGCTGAGCGCTCTAAGGCCCAACAG 828
Qy 841 CACAGTACCAAGGAGAGCCAAACCTAAGCGCGGAGAAAGTGAAGAGGCCCTTCCA 900
Db 827 CACAGTACCAAGGAGAGCCAAACCTAAGCGCGGAGAAAGTGAAGAGGCCCTTCCA 768
Qy 901 ACCTTACGCCCTTCT 960
Db 767 ACCTTACGCCCTTCT 708
Qy 961 AGGATGGAGTTTGATTTATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1020
Db 707 AGGATGGAGTTTGATTTATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 648
Qy 1021 TATTTTTCAGATGGAGTCTTGCTCTGTTTGGCCAGCTGGAGTGCAGTGGTGTGATCTCAG 1080
Db 647 TATTTTTCAGATGGAGTCTTGCTCTGTTTGGCCAGCTGGAGTGCAGTGGTGTGATCTCAG 588
Qy 1081 CTCTACTGCAACCT 1140
Db 587 CTCTACTGCAACCT 528
Qy 1141 CT 1142
Db 527 CT 526

RESULT 3

US-10-198-846-12415/c
; Sequence 12415, Application US/10198846
; Publication No. US20030099974A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Xu, Yongyao
; APPLICANT: Wang, Youzhen
; APPLICANT: Steinmann, Kathleen
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS

; TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; FILE REFERENCE: MRI-049
; CURRENT APPLICATION NUMBER: US/10198,846
; CURRENT FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/306,220
; PRIOR FILING DATE: 2001-07-18
; NUMBER OF SEQ ID NOS: 14084
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12415
; LENGTH: 2945
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-198-846-12415

Query Match 91.3%; Score 1047; DB 15; Length 2945;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1047; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GCCTTGGGTCAAGCAGAAATATTAATAGGAGGGGAATGCCTGTAGCTAGTGGGCTTA 60
Db 1673 GCCTTGGGTCAAGCAGAAATATTAATAGGAGGGGAATGCCTGTAGCTAGTGGGCTTA 1614
Qy 61 CTGCCAGCTGAGAGGAAGTGGCTCGACTCTTGACCATGGCTGGGGTTCCTGAGATGA 120
Db 1613 CTGCCAGCTGAGAGGAAGTGGCTCGACTCTTGACCATGGCTGGGGTTCCTGAGATGA 1554
Qy 121 GCTAAACCTTTCCTATGCTGCGGCTTGGAGCCACAGCATCAGATGTTGAATCAAGAA 180
Db 1553 GCTAAACCTTTCCTATGCTGCGGCTTGGAGCCACAGCATCAGATGTTGAATCAAGAA 1494
Qy 181 GGCCTATAGACAGCTGGCAGTGTGTTTCATCTGACAAAAATCATATCCCGGGCTGA 240
Db 1493 GGCCTATAGACAGCTGGCAGTGTGTTTCATCTGACAAAAATCATATCCCGGGCTGA 1434
Qy 241 GGAGCCTTCAAGGTTTTCGAGCAGCTTGGGACATGTGACAAATGCTGAAAAACGAAA 300
Db 1433 GGAGCCTTCAAGGTTTTCGAGCAGCTTGGGACATGTGACAAATGCTGAAAAACGAAA 1374
Qy 301 GGAGTATGAGATGAACGAATGGCAGAGAAATGAGCTGAGCGGTCAGTAAATGATTTCT 360
Db 1373 GGAGTATGAGATGAACGAATGGCAGAGAAATGAGCTGAGCGGTCAGTAAATGATTTCT 1314
Qy 361 GTCCAAGCTGCAAGATGACCTCAAGGAGGCAATGAATACTATGATGTGACCGATGCCA 420
Db 1313 GTCCAAGCTGCAAGATGACCTCAAGGAGGCAATGAATACTATGATGTGACCGATGCCA 1254
Qy 421 AGGAAGCATAGGAGGTTTGAATGGAACCGGGAACCTTAAGAGTGCAGATCTGTCTGA 480
Db 1253 AGGAAGCATAGGAGGTTTGAATGGAACCGGGAACCTTAAGAGTGCAGATCTGTCTGA 1194
Qy 481 GTGTAATAGGCTGCATCTCTGAGGAAGAGAGACTTTTGGGAGAGTCAAGCATGTTGGG 540
Db 1193 GTGTAATAGGCTGCATCTCTGAGGAAGAGAGACTTTTGGGAGAGTCAAGCATGTTGGG 1134
Qy 541 CCTCAAGATCACCTACTTTGACCTGAGTGGAAAGTGTATGACATCACAGAGTGGG 600
Db 1133 CCTCAAGATCACCTACTTTGACCTGAGTGGAAAGTGTATGACATCACAGAGTGGG 1074
Qy 601 TGGATGCCAGCTGTAGGTATCTCCCGAGATACCCAGAGTCCCTTATCATCTCAAT 660
Db 1073 TGGATGCCAGCTGTAGGTATCTCCCGAGATACCCAGAGTCCCTTATCATCTCAAT 1014
Qy 661 TGGTCTCGGATTCACGACCAAGAGGCGGAGAGGCCACCCAGATGCCCCCTCTCTGC 720
Db 1013 TGGTCTCGGATTCACGACCAAGAGGCGGAGAGGCCACCCAGATGCCCCCTCTCTGC 954
Qy 721 TGATCTTCAGATTTCTTGAGTGGATCTTTCAAGTACCCCGAGGAGATGCCCAATGG 780
Db 953 TGATCTTCAGATTTCTTGAGTGGATCTTTCAAGTACCCCGAGGAGATGCCCAATGG 894
Qy 781 GAATCTTCTGACGCTCCTCAGCTGCCCCCTGGAGCGGCTGCAGCTCTTAAGCCCAACAG 840

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Db 893 GAACCTTTTGGAGCTCTCTCAGCCTGCCCTGGAGCGCTGAGCCTCTAAGCCCAACAG 834
QY 841 CACAGTACCAGGAGAGCAACCTAAGCGGGGAAGAAAGTGAAGGAGGCGCCCTTCCA 900
Db 833 CACAGTACCAGGAGAGCAACCTAAGCGGGGAAGAAAGTGAAGGAGGCGCCCTTCCA 774
QY 901 AGTTGATGCCCTCTCTCTTCTCTCAATCAATGTGAGGAGTCAAAAGGGCTGTAGCAC 960
Db 773 AGTTGATGCCCTCTCTCTTCTCTCAATCAATGTGAGGAGTCAAAAGGGCTGTAGCAC 714
QY 961 AGGATGGAGTTGATTTATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1020
Db 713 AGGATGGAGTTGATTTATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 654
QY 1021 TATTTTTCAGATGGAGTCTCTCTG 1047
Db 653 TATTTTTCAGATGGAGTCTCTCTG 627

RESULT 4
US-10-096-534-43
; Sequence 43, Application US/10096534
; Publication No. US2003016887A1
; GENERAL INFORMATION:
; APPLICANT: The Brigham and Women's Hospital, Inc.
; APPLICANT: Yates, Karen
; APPLICANT: Mizuno, Shuichi
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF SKELETAL DEGENERATION CONDITIONS
; FILE REFERENCE: B0801/7244/KA/ERP
; CURRENT APPLICATION NUMBER: US/10/096,534
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: US 60/274,980
; PRIOR FILING DATE: 2001-03-12
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 43
; LENGTH: 754
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-096-534-43

Query Match 55.3%; Score 634; DB 13; Length 754;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 754; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 301 GGAGTATGAGTGAACGAATGGCAGAGAATGAGCTGAGCGGTGAGTAATGAGTTTCT 360
Db 1 GGAGTATGAGTGAACGAATGGCAGAGAATGAGCTGAGCGGTGAGTAATGAGTTTCT 60
QY 361 GTCCAAGCTGCAAGATGACCTCAAGGAGGCAATGAATACTATGATGTAGCCGATGCCA 420
Db 61 GTCCAAGCTGCAAGATGACCTCAAGGAGGCAATGAATACTATGATGTAGCCGATGCCA 120
QY 421 AGGAAAGCMTAGGAGGTTTGAATGGACCGGAACTAAGAGTGCAGATCTGTGCTGA 480
Db 121 AGGAAAGCMTAGGAGGTTTGAATGGACCGGAACTAAGAGTGCAGATCTGTGCTGA 180
QY 481 GTGTAATAGGCTGCATCTCTGCTGAGGAGGAGCTTTGGGAGGAGTCAAGCATGTTGG 540
Db 181 GTGTAATAGGCTGCATCTCTGCTGAGGAGGAGCTTTGGGAGGAGTCAAGCATGTTGG 240
QY 541 CCTCAAGATCACTACTTTGCACTGATGGATGGAAGGTGTATGACATCACAGATGGGC 600
Db 241 CCTCAAGATCACTACTTTGCACTGATGGATGGAAGGTGTATGACATCACAGATGGGC 300
QY 601 TGGATGCCAGGTGTAGGTATCTCCCGATACCCAGATGCCCTATCATCTCAT 660
Db 301 TGGATGCCAGGTGTAGGTATCTCCCGATACCCAGATGCCCTATCATCTCAT 360
QY 661 TGGTTCTGGATTCAGGCACAGAGGCGGAGAGAGCCACCCAGATGCCCTCTCTGC 720
Db 361 TGGTTCTGGATTCAGGCACAGAGGCGGAGAGAGCCACCCAGATGCCCTCTCTGC 420
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QY 721 TGATCTTCAGGATTTCTTGAGTCGGATCTTTCAAGTACCCCGAGGCGAGATGCCAATGG 780
Db 421 TGATCTTCAGGATTTCTTGAGTCGGATCTTTCAAGTACCCCGAGGCGAGATG-CCAAATGG 479
QY 781 GAACTTCTTTGCGAGCTCTCAGCCTGCCCTGGAGCGCGCTGCAGCCTCTTAAGCCCAACAG 840
Db 480 GAACTTCTTTGCGAGCTCTCAGCCTGCCCTGGAGCGCGCTGCAGCCTCTTAAGCCCAACAG 539
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QY 1021 TATTTTTCAGATGGAGTCTTGTCTCTCTTGTGCCCCAG 1055
Db 720 TATTTTTCAGATGGAGTCTTGTCTCTCTTGTGCCCCAG 754

RESULT 5
US-10-097-340-182
; Sequence 182, Application US/10097340
; Publication No. US20030087250A1
; GENERAL INFORMATION:
; APPLICANT: John MONAHAN
; APPLICANT: Manjula GANNAVAPURU
; APPLICANT: Sebastian HOERSCH
; APPLICANT: Shubhangi KAMATKAR
; APPLICANT: Steve G. KOVATS
; APPLICANT: Rachel E. MEYERS
; APPLICANT: Michael MORRISSEY
; APPLICANT: Peter OLANDT
; APPLICANT: Ami SEN
; APPLICANT: Peter VEIBY
; APPLICANT: Gordon B. MILLS
; APPLICANT: Robert C. BAST, Jr.
; APPLICANT: Karen LU
; APPLICANT: Rosemarie SCHMANDT
; APPLICANT: Xumei ZHAO
; APPLICANT: Karen GLATT
; TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification,
; FILE REFERENCE: MRI-030
; CURRENT APPLICATION NUMBER: US/10/097,340
; CURRENT FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: 60/276,025
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/325,149
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/276,026
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/324,967
; PRIOR FILING DATE: 2001/09/26
; PRIOR APPLICATION NUMBER: 60/311,732
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/325,102
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/323,580
; PRIOR FILING DATE: 2001-09-19
; NUMBER OF SEQ ID NOS: 363
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 182
; LENGTH: 754
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-097-340-182
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RESULT 6
US-09-764-891-8949
; Sequence 8949, Application US/09764891
; Publication NO. US20030077808A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC006
; CURRENT APPLICATION NUMBER: US/09/764,891
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 10231
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8949
; LENGTH: 7453

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RESULT 7
US-09-814-353-14171/c
; Sequence 14171, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; PRIOR FILING DATE: 2000-12-21
NUMBER OF SEQ ID NOS: 22037
SOFTWARE: FastSeq for Windows Version 4.0

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184 CTATAGACAGCTGGCAGTGATGGTTTCATCTCTGACAAAAATCATCATCCCCGGGCTGAGGA 243
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Qy 184 CTATAGACAGCTGGCAGTGATGGTTTCATCTCTGACAAAAATCATCATCCCCGGGCTGAGGA 243
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Qy 304 GTATGAGATGAACAGGAATGCGACAGATGAGCTGAGCCGGTCACTAGTAATGAGTTTCTGTC 363
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Qy 364 CAAGCTCAAGATGACCTCAAGGAGGCAATGAATACTATGATGTGTAGCCGATGCCAAGG 423
Db 79 CAAGCTCAAGATGACCTCAAGGAGGCAATGAATACTATGATGTGTAGCCGATGCCAAGG 20
Qy 424 AAAGCATAGGAGGTTTG 440
Db 19 AAAGCATAGGAGGTTTG 3
RESULT 9
US-09-814-353-7786/c
; Sequence 7786, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Thompson, Pamela
; APPLICANT: Lee, John
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7786
; LENGTH: 259
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; LOCATION: 1, 2_
; OTHER INFORMATION: n = A,T,C or G
US-09-814-353-7786
Query Match 22.4%; Score 257; DB 13; Length 259;
Best Local Similarity 100.0%; Pred. No. 2.5e-130;
Matches 257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 184 CTATAGACAGCTGGCAGTGATGGTTTCATCTCTGACAAAAATCATCATCCCCGGGCTGAGGA 243
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Db 199 GGCCTTCAAGGTTTTTGGAGCAGCTTTGGGACATTGTGAGCAATGTGCTGAAAAAGCGAAAGGA 140
Qy 304 GTATGAGATGAACAGGAATGCGACAGATGAGCTGAGCCGGTCACTAGTAATGAGTTTCTGTC 363
Db 139 GTATGAGATGAACAGGAATGCGACAGATGAGCTGAGCCGGTCACTAGTAATGAGTTTCTGTC 80
Qy 364 CAAGCTCAAGATGACCTCAAGGAGGCAATGAATACTATGATGTGTAGCCGATGCCAAGG 423
Db 79 CAAGCTCAAGATGACCTCAAGGAGGCAATGAATACTATGATGTGTAGCCGATGCCAAGG 20
Qy 424 AAAGCATAGGAGGTTTG 440
Db 19 AAAGCATAGGAGGTTTG 3
RESULT 9
US-09-814-353-7786/c
; Sequence 7786, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Thompson, Pamela
; APPLICANT: Lee, John
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1424
; LENGTH: 259
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; LOCATION: 1, 2_
; OTHER INFORMATION: n = A,T,C or G
US-09-814-353-1424
Query Match 22.4%; Score 257; DB 13; Length 259;
Best Local Similarity 100.0%; Pred. No. 2.5e-130;
Matches 257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 166 TGTGAAGTGAAGAGGCTATAGACAGCTGGCAGTGATGGTTTCATCTCTGACAAAAATCA 225
Db 392 TGTGAAGTGAAGAGGCTATAGACAGCTGGCAGTGATGGTTTCATCTCTGACAAAAATCA 333
Qy 226 TCATCCCCGGGCTGAGGAGCCCTTCAAGGTTTTTGGAGCAGCTTTGGGACATTGTGAGCA 285
Db 332 TCATCCCCGGGCTGAGGAGCCCTTCAAGGTTTTTGGAGCAGCTTTGGGACATTGTGAGCA 273
Qy 286 TGCTGAAAGCGAAGAGGAGTATGAGATGAACGAATGCGACAGATGAGCTGAGCCGGTC 345
Db 272 TGCTGAAAGCGAAGAGGAGTATGAGATGAACGAATGCGACAGATGAGCTGAGCCGGTC 213
Qy 346 AGTAATGAGTTTCTGTCAAGCTCAAGATGACCTCAAGGAGGCAATGAATACTATGAT 405
Db 212 AGTAATGAGTTTCTGTCAAGCTCAAGATGACCTCAAGGAGGCAATGAATACTATGAT 153
Qy 406 GTGTAGCCGATGCCAAGGAAAGCATAGGAGGTTTGA 441
Db 152 GTGTAGCCGATGCCAAGGAAAGCATAGGAGGTTTGA 117
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US-09-814-353-1424/c
; Sequence 1424, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Thompson, Pamela
; APPLICANT: Lee, John
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1424
; LENGTH: 259
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; LOCATION: 1, 2_
; OTHER INFORMATION: n = A,T,C or G
US-09-814-353-1424
Query Match 22.4%; Score 257; DB 13; Length 259;
Best Local Similarity 100.0%; Pred. No. 2.5e-130;
Matches 257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 139 GTATGAGATGAAACGAATGCGAGAGATGAGCTGAGCCGCTCAGTAAATGAGTTTCTGTC 80
Qy 364 CAAGCTGCAAGATGAGCTCAAGGAGCAATGATATCTATGATGTCGCGGATGCCAAGG 423
Db 79 CAAGCTGCAAGATGAGCTCAAGGAGCAATGATATCTATGATGTCGCGGATGCCAAGG 20
Qy 424 AAAGCATAGGAGTTTG 440
Db 19 AAAGCATAGGAGTTTG 3

RESULT 10

US-10-094-749-1448
; Sequence 1448, Application US/10094749
; Publication No. US20030219741A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHICO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA
; FILE REFERENCE: 084335/0160
; CURRENT APPLICATION NUMBER: US/10/094,749
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 60/350,435
; PRIOR FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: JP 2001-328381
; PRIOR FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 3381
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1448
; LENGTH: 2066
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-094-749-1448

Query Match 17.8%; Score 204; DB 13; Length 2066;
Best Local Similarity 100.0%; Pred. No. 3.7e-10;
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 944 CAAAAGGGCTGTAGCACAGATGGAGTTGATTTATCCCTCCTCCGCCAACACCTAGGAA 1003
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Qy 1004 CTGAATCTTTTCTTTTATTTTGTAGATGGAGTCTTCTCTGTGTCCCGAGCTGGAGTG 1063
Db 1164 CTGAATCTTTTCTTTTATTTTGTAGATGGAGTCTTCTCTGTGTCCCGAGCTGGAGTG 1223
Qy 1064 CAGTGTGTGATCTCAGCTTACTGCAACCTCTGTCTCCGGGTTCAGCAATTCCTCCAT 1123
Db 1224 CAGTGTGTGATCTCAGCTTACTGCAACCTCTGTCTCCGGGTTCAGCAATTCCTCCAT 1283
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Db 1284 CTCAGCCTCCTCAGTAGCTGGGAT 1307

RESULT 11

US-09-867-701-8500

; Sequence 8500, Application US/09867701
; Patent No. US20020132237A1
; GENERAL INFORMATION:
; APPLICANT: Aglate, Paul A.
; APPLICANT: Jones, Robert
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.497
; CURRENT APPLICATION NUMBER: US/09/867,701
; CURRENT FILING DATE: 2001-05-29
; NUMBER OF SEQ ID NOS: 10912
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8500
; LENGTH: 339
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-867-701-8500

Query Match 11.3%; Score 130; DB 10; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.6e-60;
Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 899 CAACGTTGATGCCCTTCTCTTCTCAAAATCAATGTCTCAGGAGTCAAAAGGGCTGTAGC 958
Db 26 CAACGTTGATGCCCTTCTCTTCTCAAAATCAATGTCTCAGGAGTCAAAAGGGCTGTAGC 85
Qy 959 ACAGGATGGAGTTGATTTATCCCTCCTCCCAACACCTAGGACTGAATCTTTCTT 1018
Db 86 ACAGGATGGAGTTGATTTATCCCTCCTCCCAACACCTAGGAACTGAATCTTTCTT 145
Qy 1019 TTTATTTT 1028
Db 146 TTTATTTT 155

RESULT 12

US-10-228-406A-10
; Sequence 10, Application US/10228406A
; Publication No. US20030104612A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Xuemei
; APPLICANT: Zylberth, Gabriele
; TITLE OF INVENTION: GENERATION OF TYPE I/TYPE II HYBRID FORM OF BOVINE
; TITLE OF INVENTION: VIRAL DIARRHEA VIRUS FOR USE AS VACCINE
; FILE REFERENCE: PC11051A
; CURRENT APPLICATION NUMBER: US/10/228,406A
; CURRENT FILING DATE: 2002-08-27
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 12572
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Hybrid BVD virus NADL890
US-10-228-406A-10

Query Match 7.8%; Score 89; DB 15; Length 12572;
Best Local Similarity 79.8%; Pred. No. 6.5e-38;
Matches 71; Conservative 18; Mismatches 0; Indels 0; Gaps 0;
Qy 422 GGAAGCATAGGAGTTTGAATGACCGGGAACCTAAGAGTGCCAGATCTGTCTGAG 481
Db 5006 GGAAGCAUAGGAGGUUGAUAUGACCGGGAACCUAAGAGUGCCAGAUACUGUGCUGAG 5065
Qy 482 TGTAATAGGCTGCATCTCTGTGAGGAAGG 510
Db 5066 UGUAAUAGGCTGCAUCCUGCUGAGGAAGG 5094

RESULT 13

US-10-134-288-1

; Sequence 1, Application US/10134288
; Publication No. US20030165520A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4106
; LENGTH: 510
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 32
; OTHER INFORMATION: n = A,T,C or G
; US-09-814-353-4106

Query Match 7.0%; Score 80; DB 13; Length 510;
Best Local Similarity 99.2%; Pred. No. 5e-33; Indels 0; Gaps 0;
Matches 130; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCCTTGGGTCACAGCAGATATTATAGGAGGAGGAAATGACCTGTAGCTAGTGGGCGCTA 60
Db 163 GCCTTGGGTCACAGCAGATATTATAGGAGGAGGAAATGACCTGTAGCTAGTGGGCGCTA 104

Qy 61 CTGCCAGCCTGAAGAGAAAGTGGCTCGACTCTTTGACCATGGCTGFGGTTCTCTGAGGATGA 120
Db 103 CTGCCAGCCTGGAGAGGAAGTGGCTCGACTCTTTGACCATGGCTGFGGTTCTCTGAGGATGA 44

Qy 121 GCTAAACCCCTT 131
Db 43 GCTAAACCCCTT 33

Search completed: December 22, 2003, 21:21:26
Job time : 407 secs

; Sequence 1, Application US/10134288
; Publication No. US20030165520A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Xuemei
; APPLICANT: Sheppard, Mike
; TITLE OF INVENTION: ATTENUATED FORMS OF BOVINE VIRAL DIARRHEA VIRUS
; FILE REFERENCE: PC10435A
; CURRENT APPLICATION NUMBER: US/10/134,288
; CURRENT FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: US/09/702,330
; PRIOR FILING DATE: 2000-10-31
; PRIOR APPLICATION NUMBER: 09/433,262
; PRIOR FILING DATE: 1999-11-04
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 14078
; TYPE: DNA
; ORGANISM: Bovine Viral Diarrhea Virus
; US-10-134-288-1

Query Match 7.8%; Score 89; DB 13; Length 14078;
Best Local Similarity 100.0%; Pred. No. 6.5e-38; Indels 0; Gaps 0;
Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 422 GGAAGCATAGAGGTTTGAATGACCGGAACTAAGAGTGCAGATACCTGTGCTGAG 481
Db 4550 GGAAGCATAGAGGTTTGAATGACCGGAACTAAGAGTGCAGATACCTGTGCTGAG 4609

Qy 482 TGTATAGGCTGCATCTCTGCTGAGGAGG 510
Db 4610 TGTATAGGCTGCATCTCTGCTGAGGAGG 4638

RESULT 14
US-10-228-406A-9
; Sequence 9, Application US/10228406A
; Publication No. US20030104612A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Xuemei
; APPLICANT: Zysarth, Gabriele
; TITLE OF INVENTION: GENERATION OF TYPE I/TYPE II HYBRID FORM OF BOVINE
; TITLE OF INVENTION: VIRAL DIARRHEA VIRUS FOR USE AS VACCINE
; FILE REFERENCE: PC11051A
; CURRENT APPLICATION NUMBER: US/10/228,406A
; CURRENT FILING DATE: 2002-08-27
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 16713
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pNADL890 vector
; US-10-228-406A-9

Query Match 7.8%; Score 89; DB 15; Length 16713;
Best Local Similarity 100.0%; Pred. No. 6.6e-38; Indels 0; Gaps 0;
Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 422 GGAAGCATAGAGGTTTGAATGACCGGAACTAAGAGTGCAGATACCTGTGCTGAG 481
Db 5006 GGAAGCATAGAGGTTTGAATGACCGGAACTAAGAGTGCAGATACCTGTGCTGAG 5085

Qy 482 TGTATAGGCTGCATCTCTGCTGAGGAGG 510
Db 5066 TGTATAGGCTGCATCTCTGCTGAGGAGG 5094

RESULT 15
US-09-814-353-4106/c
; Sequence 4106, Application US/09814353
; Publication No. US20030165831A1

OM nucleic - nucleic search, using sw model
Run on: December 22, 2003, 17:14:33 : Search time 2750. Seconds
(without alignments)
10137.176 Million cell updates/sec

Title: US-10-049-742-22
Perfect score: 1147
Sequence: 1 gctctgggtcaacagagaata.....gctctctgagtagctgggat 1147

Scoring table: OLIGO NUC
Gapop 60.0 , Gapext 60.0
Searched: 22781392 seqs, 12152238056 residues

Word size : 0
Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : EST:
1: em_estba:*
2: em_esthum:*
3: em_esthum:*
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5: em_esthum:*
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16: em_estfun:*
17: em_gss_hum:*
18: em_gss_hum:*
19: em_gss_hum:*
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24: em_gss_vrt:*
25: em_gss_vrt:*
26: em_gss_vrt:*
27: em_gss_vrt:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	704	61.4	918	13	BU956189
2	692	60.3	957	12	BM802135
3	663	57.8	942	13	BU538214
4	639	55.7	906	10	BM676002

5	635	55.4	878	12	BG763500
6	635	55.4	995	12	BM452174
7	622	54.2	1046	12	BM802913
8	607	52.9	904	13	BQ691177
9	605	52.7	605	13	BX090711
10	585	51.0	955	13	BU538351
11	565	49.3	1046	12	BQ058270
12	550	48.0	618	12	BM011379
13	542	47.3	723	10	BE779250
14	509	44.4	927	12	BM424147
15	474	41.3	912	10	BG751088
16	441	38.4	723	10	BE519407
17	437	38.1	785	12	B1333110
18	423	36.9	776	12	BG821631
19	417	36.4	469	10	BG504969
20	382	33.3	968	13	B0838931
21	372	32.4	527	12	B1002288
22	366	31.9	874	10	BF679562
23	362	31.6	505	10	BF819630
24	348	30.3	588	9	AA460131
25	317	27.6	741	12	BG761596
26	316	27.6	448	12	B1002295
27	314	27.4	864	10	BQ252385
28	258	22.5	325	14	RI7611
29	257	22.4	621	10	BE385257
30	254	22.1	788	10	BE304441
31	248	21.6	648	13	B0629493
32	226	19.7	338	10	BF902230
33	218	19.0	704	9	AV729617
34	209	18.2	805	10	BE536083
35	207	18.0	596	12	BM823481
36	163	14.2	514	9	AI435045
37	163	14.2	928	10	BG678276
38	146	12.7	859	13	BQ225350
39	145	12.6	940	10	BG328197
40	143	12.5	786	10	BF965963
41	135	11.8	938	12	B1259675
42	130	11.3	339	9	AB908339
43	112	9.8	163	10	BE826354
44	109	9.5	843	13	BQ220945
45	91	7.9	474	13	BQ323294

ALIGNMENTS

BU956189 918 bp mRNA linear EST 21-OCT-2002
AGENCY: 10613510 NIH_MGC_107 Homo sapiens cdna clone
IMAGE: 6729715 5', mRNA sequence.
BU956189
EST: BU956189.1 GI:24185761
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 918)
NIH-MGC <http://mgi.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LICM3053 row: f column: 18
High quality sequence stop: 544.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

ORIGIN	Query Match	57.8%;	Score 663;	DB 13;	Length 942;
	Best Local Similarity	99.9%;	Pred. No. 2.1e-213;		
	Matches 713;	Conservative 0;	Mismatches- 1;	Indels 0;	Gaps 0;
QY	182	GCCTATAGACAGCTGSCAGTGATGTTTCATCTCTGACAAAAATCATCATCCCGCGGCTGAG	241		
Db	1	GCCTATAGACAGCTGSCAGTGATGTTTCATCTCTGACAAAAATCATCATCCCGCGGCTGAG	60		
QY	242	GAGGCCCTTCAAGGTTTTTGGAGCAGCTTGGGACATTTGTACGAAATGCTGAAAAAGCGAAAG	301		
Db	61	GAGGCCCTTCAAGGTTTTTGGAGCAGCTTGGGACATTTGTACGAAATGCTGAAAAAGCGAAAG	120		
QY	302	GAGTATGAGATGAAACGAAATGGCAGAGAAATGAGCTGAGCCGGTCAGTAAATGAGTTTCTG	361		
Db	121	GAGTATGAGATGAAACGAAATGGCAGAGAAATGAGCTGAGCCGGTCAGTAAATGAGTTTCTG	180		
QY	362	TCCAAAGCTCAAGATGACCTCAAGGAGGCAATGAATACTATGATGTGTAGCCGATGCCAA	421		
Db	181	TCCAAAGCTCAAGATGACCTCAAGGAGGCAATGAATACTATGATGTGTAGCCGATGCCAA	240		
QY	422	GGAAAGCATAGGAGTTTTGAAATGGACCGGGAACCTTAAGAGTGCCAGATACTGTGCTGAG	481		
Db	241	GGAAAGCATAGGAGTTTTGAAATGGACCGGGAACCTTAAGAGTGCCAGATACTGTGCTGAG	300		

301	TGTAATAGGCTGCATCCTGCTGAGGAAGGAC	TTTGGGCAGAGTCAAGCATGTTGGGC	360
542	CTCAGATCACCCTACTTTTGCACTGATGATGGAAGGTGTA	TGATCATCACAGATGGGCT	601
361	CTCAAGATCACCCTACTTTTGCACTGATGATGGAAGGTGTA	TGATCATCACAGATGGGCT	420
602	GGATGCCAGCGTGTAGGTATCTCCCCAGATACCCACAGAGT	CCCCCTATCATCTCTCATTT	661
421	GGATGCCAGCGTGTAGGTATCTCCCCAGATACCCACAGAGT	CCCCCTATCATCTCTCATTT	480
662	GGTTCTCGGATTCAGAGGCCAGAGGGCGGCAGAGAGCCACC	CCAGATGCCCCCTCTCTGCT	721
481	GGTTCTCGGATTCAGAGGCCAGAGGGCGGCAGAGAGCCACC	CCAGATGCCCCCTCTCTGCT	540
722	GATCTTCAGGATTTCTTGAGTCGGATCTTCTCAAGTACCC	CCAGGGCAGATGCCCAATGGG	781
541	GATCTTCAGGATTTCTTGAGTCGGATCTTCTCAAGTACCC	CCAGGGCAGATGCCCAATGGG	600
782	AACTTCTTTGAGCTCCTCAGCGCTGCCCTGGAGCGCGCTGC	AGGCTCTAAGGCCCAACAGC	841
601	AACTTCTTTGAGCTCCTCAGCGCTGCCCTGGAGCGCGCTGC	AGGCTCTAAGGCCCAACAGC	660
842	ACAGTACCCAGGGAGAGCCAAACCTTAAGCGGCGGAAGAA	AGTGAAGAGGCGCC	895
661	ACAGTACCCAGGGAGAGCCAAACCTTAAGCGGCGGAAGAA	AGTGAAGAGGCGCC	714

RESULT 4	906 bp	linear	EST 01-MAY-2001
BG676002	906 bp	mrna	
LOCUS	906 bp	mrna	
DEFINITION	602622366F1 NCI_CGAP_Skn4 Homo sapiens cDNA clone IMAGE:4747337 5', mrna sequence..		
ACCESSION	BG676002		
VERSION	BG676002.1 GI:13907398		
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	1 (bases 1 to 906)		
TITLE	NIH-MGC http://mgc.nci.nih.gov/ .		
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)		
COMMENT	Unpublished		
	Contact: Robert Strausberg, Ph.D.		
	Email: cgapbs-r@mail.nih.gov		

Db 361 GTAGGTATCTCCCCAGATACCCACAGAGTCCCTCATCATCTCAATTTGGTTCTGGATT 420
QY 674 CCAGGCACAGAGGCGGCAGAGAGCCACCCAGATGCCCTCTCTGCTGATCTTCAGGAT 733
Db 421 CCAGGCACAGAGGCGGCAGAGAGCCACCCAGATGCCCTCTCTGCTGATCTTCAGGAT 480
QY 734 TTCTTGAGTGGGATCTTTCAAGTACCCCCAGGCGAGATGCCCAATGGGAACTTCTTTGCA 793
Db 481 TTCTTGAGTGGGATCTTTCAAGTACCCCCAGGCGAGATGCCCAATGGGAACTTCTTTGCA 540
QY 794 GTCCTCAGCCTGCCCTGGAGCGGCTGCAGGCTCTAAGCCCAACAGCAGATACCCCAAG 853
Db 541 GTCCTCAGCCTGCCCTGGAGCGGCTGCAGGCTCTAAGCCCAACAGCAGATACCCCAAG 600
QY 854 GGAGAAG 860
Db 601 GGAGAAG 607

RESULT 9
BX090711
LOCUS BX090711 Soares_total_fetus_Nb2HF8 9w Homo sapiens cDNA clone EST 23-JAN-2003
DEFINITION IMAGp998P081964 ; IMAGE:796663, mRNA sequence.

ACCESSION BX090711
VERSION BX090711.1 GI:27826181
KEYWORDS EST.
SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 605)

Ebert,L., Heil,O., Hennig,S., Neubert,P., Partsch,E., Peters,M.,

Radelof,U., Schneider,D. and Korn,B.

Human Unigeneset - RZPD3

Unpublished

Contact: Ina Rolfs

RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH

Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany

RZPD; IMAGp998P081964.

RZPDLIB; I.M.A.G.E. cDNA Clone Collection;

Human Unigeneset - RZPD3 (RZPDLIB No.972);

http://www.rzpd.de/cloneCards/cgi-

bin/showLib.pl.cgi/response?libNo=972 Contact: Ina Rolfs

RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH

Heubnerweg 6, D-14059 Berlin, Germany

Tel: +49 30 32639 101

Fax: +49 30 32639 111

www.rzpd.de

This clone is available royalty-free from RZPD;

contact RZPD (clone@rzpd.de) for further information. Seq primer:

M13r, Primer sequence: TTTCACAGGAAACAGCTATGAC.

Location/Qualifiers

1. 605

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGp998P081964 ; IMAGE:796663"

/dev_stage="8-9 weeks"

/lab_host="DH10B"

/clone_lib="Soares_total_fetus Nb2HF8 9w"

/note="Vector: p773D-Pac (Pharmacia) with a modified

polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA

was prepared from mRNA obtained from pooled 8-9 week

(total) fetus material with a Not I - oligo(dT) primer [5'

TGTTACCAATGAGTGGAGCGGCGCTAATTTTTTTTTTTT 3'].

Double-stranded cDNA was ligated to Eco RI adaptors

(Pharmacia), digested with Not I and cloned into the Not I

and Eco RI sites of the modified p773 vector. Library

went through one round of normalization, and was

constructed by Bento Soares and M. Fatima Bonaldo. "

140 a 162 c 155 g 148 t

BASE COUNT

ORIGIN

Query Match 52.7%; Score 605; DB 13; Length 605;
Best Local Similarity 100.0%; Pred. No. 7.8e-194;
Matches 605; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 466 CAGATACGTGCTGAGTGTAAATAGGCTGCATCTCTGCTGAGAAAGAGACATTTTGGGCAGA 525
Db 1 CAGATACTGTGCTGAGTGTAAATAGGCTGCATCTCTGCTGAGAAAGAGACATTTTGGGCAGA 60
QY 526 GTCAGCATGTTGGGCTCAAGATCACCTACTTTTGCATCTGATGGATGGAAGGTGTATGA 585
Db 61 GTCAGCATGTTGGGCTCAAGATCACCTACTTTTGCATCTGATGGATGGAAGGTGTATGA 120
QY 586 CATCACAGAGTGGGCTGGATGCCAGGCTGAGGTATCTCCCCAGATACCCACAGAGTCCC 645
Db 121 CATCACAGAGTGGGCTGGATGCCAGGCTGAGGTATCTCCCCAGATACCCACAGAGTCCC 180
QY 646 CTATCATCTCTATTTGGTTCTCGGATTCAGAGCCAGAGGGCGGAGAGACACCCC 705
Db 181 CTATCATCTCTATTTGGTTCTCGGATTCAGAGCCAGAGGGCGGAGAGACACCCC 240
QY 706 AGATGCCCCCTCTGCTGATCTTCAGGATTTCTTGAFTCGGATCTTTCAAGTACCCCCAGG 765
Db 241 AGATGCCCCCTCTGCTGATCTTCAGGATTTCTTGAFTCGGATCTTTCAAGTACCCCCAGG 300
QY 766 GCAGATGCCCAATGGGAACTTCTTTGAGCTCTCAGCTGCCCTGGAGCCCGCTGCAGC 825
Db 301 GCAGATGCCCAATGGGAACTTCTTTGAGCTCTCAGCTGCCCTGGAGCCCGCTGCAGC 360
QY 826 CTCTAAGCCCAACAGACAGTACCCAGGAGAGCCAACTTAAGCGCGGAGAGAAAGT 885
Db 361 CTCTAAGCCCAACAGACAGTACCCAGGAGAGCCAACTTAAGCGCGGAGAGAAAGT 420
QY 886 GAGGAGGCCCTTCCAACTGATGCCCTTCTCTTCTCTCAAAATCAATGTCAAGGAGTCA 945
Db 421 GAGGAGGCCCTTCCAACTGATGCCCTTCTCTTCTCTCAAAATCAATGTCAAGGAGTCA 480
QY 946 AAGGGCTGTAGCACAGGATGGAGTTTGAATTTATCCCTCTCCCTCCCAACACCTAGGAAC 1005
Db 481 AAGGGCTGTAGCACAGGATGGAGTTTGAATTTATCCCTCTCCCTCCCAACACCTAGGAAC 540
QY 1006 GAATCTTTTCTTTTATTTTGTGATGGAGTCTTGTCTGTTCCTGCTGAGTCA 1065
Db 541 GAATCTTTTCTTTTATTTTGTGATGGAGTCTTGTCTGTTCCTGCTGAGTCA 1065
QY 1066 GTGGT 1070
Db 601 GTGGT 605

RESULT 10

BUS38351

LOCUS

DEFINITION

AGENCOURT_10181238 NIH_MGC_107 Homo sapiens cDNA clone

IMAGE:6568891 5', mRNA sequence.

ACCESSION

BUS38351

VERSION

BUS38351.1 GI:22848792

KEYWORDS

EST.

SOURCE

Homo sapiens

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 955)

NIH-MGC http://mgi.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished

CONTACT: Robert Strausberg, Ph.D.

Email: cgabbs@mail.nih.gov

Tissue Procurement: ARCC

cDNA Library Preparation: Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2755 row: e column: 19
High quality sequence stop: 583.
Location/Qualifiers

FEATURES
source

1. .955
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:658891"
/tissue_type="adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_107"
/notes="Organ: breast; Vector: pOTB7; Site_1: EcoRI;
Site_2: XhoI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
239 a 241 c 261 g 213 t 1 others

Query Match 51.0%; Score 585; DB 13; Length 955;
Best Local Similarity 100.0%; Pred. No. 48-187;
Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 182 GCCTATAGACAGCTGGCAGTGATGGTTTCCTCGACAAATAATCATATCCCCGGGCTGAG 241
Db 1 GCCTATAGACAGCTGGCAGTGATGGTTTCCTCGACAAATAATCATATCCCCGGGCTGAG 60
QY 242 GAGGCTTCAAGTTTTCGAGCAGCTTGGGACATTTGTGACAAATCTGAAAAAGCAAAG 301
Db 61 GAGGCTTCAAGTTTTCGAGCAGCTTGGGACATTTGTGACAAATCTGAAAAAGCAAAG 120
QY 302 GACTATGAGATGAACGAATGGCAGAGATGACTGAGCGGTTCAGTAAATGATGTTCTG 361
Db 121 GACTATGAGATGAACGAATGGCAGAGATGACTGAGCGGTTCAGTAAATGATGTTCTG 180
QY 362 TCCAAGCTGCAAGTACCTCAAGGAGCAATGAATACTATGATGTGACCGCATGCCAA 421
Db 181 TCCAAGCTGCAAGTACCTCAAGGAGCAATGAATACTATGATGTGACCGCATGCCAA 240
QY 422 GGAAGCATAGGAGTTTGAATGGACCGGAACTTAAGAGTGCCAGATCTGTGCTGAG 481
Db 241 GGAAGCATAGGAGTTTGAATGGACCGGAACTTAAGAGTGCCAGATCTGTGCTGAG 300
QY 482 TGTAAATAGCTGCATCTCTGAGGAGGAGACTTTTGGCAGAGTCAAGCATGTTGGGC 541
Db 301 TGTAAATAGCTGCATCTCTGAGGAGGAGACTTTTGGCAGAGTCAAGCATGTTGGGC 360
QY 542 CTCAAGATCACCTACTTTGCACGTGATGGTGAAGGTGTATGACATCAGAGTGGCT 501
Db 361 CTCAAGATCACCTACTTTGCACGTGATGGTGAAGGTGTATGACATCAGAGTGGCT 420
QY 602 GGATGCGAGCGTGTAGGTATCTCCCGAGATACCCACAGAGTCCCTCATCATCTCATTT 661
Db 421 GGATGCGAGCGTGTAGGTATCTCCCGAGATACCCACAGAGTCCCTCATCATCTCATTT 480
QY 662 GGTTCCTCGAATCCAGGACCAAGGCGGCGAGAGCCACCCAGATGCCCTCTCTGCT 721
Db 481 GGTTCCTCGAATCCAGGACCAAGGCGGCGAGAGCCACCCAGATGCCCTCTCTGCT 540
QY 722 GATCTTCAGAGTTCTTGAGTCGGATCTTCAAGTACCCCGG 766
Db 541 GATCTTCAGAGTTCTTGAGTCGGATCTTCAAGTACCCCGG 585

RESULT 11
BQ058270
LOCUS
DEFINITION BQ058270 1046 bp mRNA linear EST 29-MAR-2002
AGENCOURT_6794554 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:5814097

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

BQ058270
BQ058270.1 GI:19817610
EST.
Homo sapiens (human)
Mammalia; Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1046)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: Lou Staudt
cDNA Library Preparation: Rubin Laboratory
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2667 row: d column: 02
High quality sequence stop: 626.
Location/Qualifiers

FEATURES
source

1. .1046
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5814097"
/tissue_type="lymphoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_99"
/notes="Organ: lymph; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
Library."
232 a 298 c 251 g 265 t

Query Match 49.3%; Score 565; DB 12; Length 1046;
Best Local Similarity 100.0%; Pred. No. 2.2e-180;
Matches 565; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 583 TGACATCAGAGTGGGCTGGATGCCGCTGTAGGTATCTCCCGAGATACCCACAGAGT 642
Db 1 TGACATCAGAGTGGGCTGGATGCCGCTGTAGGTATCTCCCGAGATACCCACAGAGT 60
QY 643 CCCCTATCACATCTCATTTGGTTCTCGGATTCAGGACCCAGAGGGCGGAGAGCCAC 702
Db 61 CCCCTATCACATCTCATTTGGTTCTCGGATTCAGGACCCAGAGGGCGGAGAGCCAC 120
QY 703 CCCAGATGCCCTCTCTGCTGATCTTCAGGATTTCTTGAGTCGGATCTTTCAAGTACCC 762
Db 121 CCCAGATGCCCTCTCTGCTGATCTTCAGGATTTCTTGAGTCGGATCTTTCAAGTACCC 180
QY 763 AGGCGAGATGCCAATGGGAACTTCTTTGACGCTCCTCAGCTCCTCCCTGAGCGCGTGC 822
Db 181 AGGCGAGATGCCAATGGGAACTTCTTTGACGCTCCTCAGCTCCTCCCTGAGCGCGTGC 240
QY 823 AGCTCTTAAGCCCAACAGCAGTACCCAAAGGAGAGCCAAACCTAAGCGCGCGAAGAA 882
Db 241 AGCTCTTAAGCCCAACAGCAGTACCCAAAGGAGAGCCAAACCTAAGCGCGCGAAGAA 300
QY 883 AGTGAGGAGGCCCTTCCAAACGTTGATGCCCTTCTTTTCTTCTCAATCAATGTGAGGAG 942
Db 301 AGTGAGGAGGCCCTTCCAAACGTTGATGCCCTTCTTTTCTTCTCAATCAATGTGAGGAG 360
QY 943 TCAAAAGGGCTGTAGCAGCAGATGGATTTGATTTATCCCTCTCTCCCGACACCTAGGA 1002

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Db 361 TCAAAAGGCGTGTAGCAGAGTGGAGTTTGAATTTATCCCTCCCTCCCAACACCTAGGA 420
QY 1003 ACTGAATCTTTTCTTTTATTTTATTTTGTAGATGGAGTCTGTCTGTGCCCAGCTGAGT 1062
Db 421 ACTGAATCTTTTCTTTTATTTTATTTTGTAGATGGAGTCTGTCTGTGCCCAGCTGAGT 480
QY 1063 GCAGTGGTGTGATCTCAGCTTACTGCAACCTCTGTCTCCCGGGTTCAAGCAATTTCTCCCA 1122
Db 481 GCAGTGGTGTGATCTCAGCTTACTGCAACCTCTGTCTCCCGGGTTCAAGCAATTTCTCCCA 540
QY 1123 TCTCAGCTCTCTGAGTAGCTGGGAT 1147
Db 541 TCTCAGCTCTCTGAGTAGCTGGGAT 565

RESULT 12
BM011379
LOCUS 603635574F1 NIH_MGC_47 Homo sapiens cDNA clone IMAGE:5457763 5',
DEFINITION mRNA sequence.
ACCESSION BM011379.1 GI:16525733
VERSION EST.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 618)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LICM1958 row: d column: 20
High quality sequence stop: 618.
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/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_47"
/note="Organ: brain; Vector: pOT87; Site 1: XhoI; Site 2:
EcoRI; CDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCAAGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH MGC Library."
BASE COUNT 168 a 119 c 197 g 134 t
ORIGIN
source

Query Match 48.0%; Score 550; DB 12; Length 618;
Best Local Similarity 100.0%; Pred. No. 2.6e-175;
Matches 550; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCTTGGCTCAACAGATTTAATAGGACGGGGAATGCACCTGTAGCTAGTGGCGCTA 60
Db 69 GCCTTGGCTCAACAGATTTAATAGGACGGGGAATGCACCTGTAGCTAGTGGCGCTA 128
QY 61 CTGCCAGCCTGAAGAGGAGTGGCTCGACTCTTTGACCATGGCTGGGTTCCCTGAGGATGA 120
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Db 129 CTGCCAGCCTGAAGAGGAGTGGCTCGACTCTTTGACCATGGCTGGGTTCCCTGAGGATGA 188
QY 121 GCTAAACCCCTTTCCATGTACTGTGGGGTTGAGGCCACAGCATCAGATGTTGAACCTGAAGAA 180
Db 189 GCTAAACCCCTTTCCATGTACTGTGGGGTTGAGGCCACAGCATCAGATGTTGAACCTGAAGAA 248
QY 181 GGCTTATAGACAGCTGCGCAGTGTGTTTCATCTGACAAAATCATCATCCCCGGGCTGA 240
Db 249 GGCTTATAGACAGCTGCGCAGTGTGTTTCATCTGACAAAATCATCATCCCCGGGCTGA 308
QY 241 GGAGGCGCTTCAAGGTTTTCGAGCAGCTTGGGACATTTGTCAAGCAATGCTGAAAAGCGAAA 300
Db 309 GGAGGCGCTTCAAGGTTTTCGAGCAGCTTGGGACATTTGTCAAGCAATGCTGAAAAGCGAAA 368
QY 301 GGAGTATGAGATGAACAGAAATGGCAGAGATGAGTGAGCCGGTCACTAAATGAGTTTCT 360
Db 369 GGAGTATGAGATGAACAGAAATGGCAGAGATGAGTGAGCCGGTCACTAAATGAGTTTCT 428
QY 361 GTCCAGAGCTGCAAGATGACCTCAAGGAGCAATGAATCTATGATGTGTAGCCGATGCCA 420
Db 429 GTCCAGAGCTGCAAGATGACCTCAAGGAGCAATGAATCTATGATGTGTAGCCGATGCCA 488
QY 421 AGGAAAGCATAGGAGGTTTGAATGGACCGGGAACCTTAGAGTGCCAGATCTGTGCTGA 480
Db 489 AGGAAAGCATAGGAGGTTTGAATGGACCGGGAACCTTAGAGTGCCAGATCTGTGCTGA 548
QY 481 GTGTAATAGCTGCATCTCTGCTGAGGAAGGAGACTTTTGGGAGAGTCAAGCATGTTGGG 540
Db 549 GTGTAATAGCTGCATCTCTGCTGAGGAAGGAGACTTTTGGGAGAGTCAAGCATGTTGGG 608
QY 541 CCTCAAGATC 550
Db 609 CCTCAAGATC 618

RESULT 13
BM011379
LOCUS 601464514F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3867794 5',
DEFINITION mRNA sequence.
ACCESSION BE779250
VERSION BE779250.1 GI:10200448
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 723)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9614 row: 1 column: 03
High quality sequence stop: 643.
Location/Qualifiers
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/clone_lib="NIH_MGC_67"
/note="Organ: eye; Vector: pCMV-SPORT6; Site 1: NotI;
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Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.75 kb. Library constructed by Life Technologies.
BASE COUNT 201 a 162 c 208 g 152 t
ORIGIN

Query Match 47.3%; Score 542; DB 10; Length 723;
Best Local Similarity 100.0%; Pred. No. 1.3e-172; Indels 0; Gaps 0;
Matches 542; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 163 AGATGTTGAACCTGAAGAAGCCTATAGACAGCTGGCAGTGATGGTTTCATCTCTGACAAAAA 222
DB 1 AGATGTTGAACCTGAAGAAGCCTATAGACAGCTGGCAGTGATGGTTTCATCTCTGACAAAAA 60

QY 223 TCATCATCCCGGGCTGAGGAGCCCTCAAGGTTTTCGAGCAGCTTGGGACATTGTCTAG 282
DB 61 TCATCATCCCGGGCTGAGGAGCCCTCAAGGTTTTCGAGCAGCTTGGGACATTGTCTAG 120

QY 283 CAATGCTGAAAACGCGAAGAGATGATGAGATGAAACCAATGGCAGAGAATGAGTGGCCG 342
DB 121 CAATGCTGAAAACGCGAAGAGATGATGAGATGAAACCAATGGCAGAGAATGAGTGGCCG 180

QY 343 GTCAGTAAATGAGTTTCTGTCCAGCTGCAAGATGACCTCAAGGAGGCAATGAATACTAT 402
DB 181 GTCAGTAAATGAGTTTCTGTCCAGCTGCAAGATGACCTCAAGGAGGCAATGAATACTAT 240

QY 403 GATGTTAGCCGATGCCAAGGAAAGCATAGGAGTTTGAATGGACCGGAACCTTAAGAG 462
DB 241 GATGTTAGCCGATGCCAAGGAAAGCATAGGAGTTTGAATGGACCGGAACCTTAAGAG 300

QY 463 TGGCAGATAGTGTGAGTGTAATAGGCTGCATCTGCTGAGGAGGAGACTTTTGGGC 522
DB 301 TGGCAGATAGTGTGAGTGTAATAGGCTGCATCTGCTGAGGAGGAGACTTTTGGGC 360

QY 523 AGAGTCAAGCATGTTGGGCTCAAGATCACCTACTTTGCACTGATGGATGGAAGGTGTA 582
DB 361 AGAGTCAAGCATGTTGGGCTCAAGATCACCTACTTTGCACTGATGGATGGAAGGTGTA 420

QY 583 TGACATCACAGATGGGCTGGATGCCAGCGTGATGATCTCCCCAGATACCCACAGAGT 642
DB 421 TGACATCACAGATGGGCTGGATGCCAGCGTGATGATCTCCCCAGATACCCACAGAGT 480

QY 643 CCCTATACATCTCAATTTGGTTCTCGATTCAGGACACAGAGGCGGACAGAGCCAC 702
DB 481 CCCTATACATCTCAATTTGGTTCTCGATTCAGGACACAGAGGCGGACAGAGCCAC 540

QY 703 CC 704
DB 541 CC 542

RESULT 14
BM424147
LOCUS
DEFINITION AGENCOURT_6398639 NIH_MGC_41 Homo sapiens cDNA clone IMAGE:5517411
5', mRNA sequence.
BM424147
BM424147.1 GI:18392359
EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 927)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Plate: LUCM2019 row: j column: 04
High quality sequence stop: 460.
Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5517411"
/tissue_type="amelanotic melanoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_41"
/note="Organ: skin; Vector: pOTB7; Site: 1: XhoI; Site: 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACAGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH MGC Library."
BASE COUNT 236 a 241 c 245 g 204 t 1 others
ORIGIN

Query Match 44.4%; Score 509; DB 12; Length 927;
Best Local Similarity 100.0%; Pred. No. 1.6e-161;
Matches 509; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 209 CATCTGCAAAAATCATCTCCCGGCTGAGGAGCCCTCAAGGTTTTCGAGCAGCT 268
DB 27 CATCTGCAAAAATCATCTCCCGGCTGAGGAGCCCTCAAGGTTTTCGAGCAGCT 86

QY 259 TGGGACATTTGTGAGCAATGCTGAAAAGCGAAAGAGATGAGATGAAACGAATGGCAGAG 328
DB 87 TGGGACATTTGTGAGCAATGCTGAAAAGCGAAAGAGATGAGATGAAACGAATGGCAGAG 146

QY 329 AATGAGCTGAGCCCGTCAAGTAAATGAGTTTCTGCCAAGCTGCAAGATGACCTCAAGGAG 388
DB 147 AATGAGCTGAGCCCGTCAAGTAAATGAGTTTCTGCCAAGCTGCAAGATGACCTCAAGGAG 206

QY 389 GCAATGAATACTATGATGTGTAGCCGATGCCAAGAAAGCATAGAGGTTTGAATGGAC 448
DB 207 GCAATGAATACTATGATGTGTAGCCGATGCCAAGAAAGCATAGAGGTTTGAATGGAC 266

QY 449 CGGGAACCTAGAGTGGCAGATCTGTGCTGAGTGTAAATAGGCTGCATCTCTGCTGAGGAA 508
DB 257 CGGGAACCTAGAGTGGCAGATCTGTGCTGAGTGTAAATAGGCTGCATCTCTGCTGAGGAA 326

QY 509 GGAGACTTTTGGGAGAGTCAAGCATGTTGGGCTCAAGATCACTACTTTGCACTGATG 568
DB 327 GGAGACTTTTGGGAGAGTCAAGCATGTTGGGCTCAAGATCACTACTTTGCACTGATG 386

QY 569 GATGAAAAGGTGTATGACATCAGAGTGGGCTGGATGCCAGCGTGTAGGTATCTCCCA 628
DB 387 GATGAAAAGGTGTATGACATCAGAGTGGGCTGGATGCCAGCGTGTAGGTATCTCCCA 446

QY 629 GATACCCACAGAGTCCCTATCATCTCTATTTGGTTCTCGGATTCAGGACACAGAGG 688
DB 447 GATACCCACAGAGTCCCTATCATCTCTATTTGGTTCTCGGATTCAGGACACAGAGG 506

QY 689 CGGAGAGAGCCACCCAGAGTGCCTCC 717
DB 507 CGGAGAGAGCCACCCAGAGTGCCTCC 535

RESULT 15
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LOCUS
DEFINITION BG751088 912 bp mRNA linear EST 15-MAY-2001
602729879F1 NIH_MGC_43 Homo sapiens cDNA clone IMAGE:4873555 5', mRNA sequence.
BG751088
ACCESSION BG751088
VERSION BG751088.1 GI:14061741

EST. 624 AGGAAAGCATAGGAGGTTTGAATGGACCGGAACCTAAGAGTGCCAGATCTG 677
Db
Search completed: December 22, 2003, 19:59:26
Job time : 2762 secs

KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Mammalia: Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 912)
REFERENCE NIH-MGC <http://mgc.nci.nih.gov/>.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished
JOURNAL
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLCMI751 row: n column: 20
High quality sequence stop: 778.

FEATURES
source
1..912
Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:487355"
/tissue_type="normal pigmented retinal epithelium"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_43"
/note="Organ: eye; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GCACGAG(G).. Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library. |"
BASE COUNT 225 a 191 c 288 g 208 t
ORIGIN

Query Match 41.3%; Score 474; DB 10; Length 912;
Best Local Similarity 100.0%; Pred. No. 1e-149;
Matches 474; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCCTTGGGTCAAGCAGAAATTAATAGCAGGGGAATGCACCTCTAGCTAGTGGCGCTA 60
Db |||||||
204 GCCTTGGGTCAAGCAGAAATTAATAGCAGGGGAATGCACCTCTAGCTAGTGGCGCTA 263
QY 61 CTGCCAGCCTCAAGAGGAGTGGCTCGACTCTTGACCATGGCTGGGTTCTCTGAGGATGA 120
Db |||||||
264 CTGCCAGCCTCAAGAGGAGTGGCTCGACTCTTGACCATGGCTGGGTTCTCTGAGGATGA 323
QY 121 GCTAAACCCCTTTCATGTACTGGGGTTGAGGCCACAGCATCATCTGAACTGAAGAA 180
Db |||||||
324 GCTAAACCCCTTTCATGTACTGGGGTTGAGGCCACAGCATCATCTGAACTGAAGAA 383
QY 181 GGCCTATAGACAGCTGGCAGTGTGTTTCATCTGCACAAAATCATCTCCCGGCTGA 240
Db |||||||
384 GGCCTATAGACAGCTGGCAGTGTGTTTCATCTGCACAAAATCATCTCCCGGCTGA 443
QY 241 GGAGGCTTCAAGGTTTGGAGCAGCTTGGACATTTGTGACCAATGCTGAAAAGCGAAA 300
Db |||||||
444 GGAGGCTTCAAGGTTTGGAGCAGCTTGGACATTTGTGACCAATGCTGAAAAGCGAAA 503
QY 301 GGAGTATGAGATGAAGCAATGGCAGAGAAATGAGCTGAGCCGGTCACTAAATGAGTTTCT 360
Db |||||||
504 GGAGTATGAGATGAAGCAATGGCAGAGAAATGAGCTGAGCCGGTCACTAAATGAGTTTCT 563
QY 361 GTCCAAGCTGCAAGATCACCTCAAGGAGGCAATGAATACTATGATGTGTAGCCGATGCCA 420
Db |||||||
564 GTCCAAGCTGCAAGATCACCTCAAGGAGGCAATGAATACTATGATGTGTAGCCGATGCCA 623
QY 421 AGGAAAGCATAGGAGGTTTGAATGGACCGGAACCTAAGAGTGCCAGATCTG 474